

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:28:46 ; Search time 40 Seconds  
(without alignments)  
951.663 Million cell updates/sec

Title: US-09-996-015-6  
Perfect score: 3070  
Sequence: 1 MWGLLLAALFAFAVGPALG.....GAKVPPDRLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2980	97.1	734	4	US-09-641-741-2
2	2976	96.9	734	3	US-08-706-216-2
3	2976	96.9	734	4	US-09-650-284B-2
4	2378.5	77.5	722	4	US-09-641-741-32
5	1398.5	45.6	764	4	US-09-641-741-31
6	1390.5	45.3	756	4	US-10-140-002-392
7	1180.5	38.5	1128	1	US-08-111-939-2
8	1180.5	38.5	1128	4	US-09-641-741-30
9	1180.5	38.0	1128	4	US-09-060-482-8
10	1166	38.0	845	4	US-09-641-741-29
11	1166	38.0	1158	4	US-09-060-482-2
12	1074	35.0	377	4	US-09-148-545-140
13	1071.5	34.9	719	4	US-09-641-741-28
14	1002.5	32.7	506	4	US-09-370-833-34
15	1002.5	32.7	506	4	US-09-854-133-34
16	815	26.5	208	4	US-09-148-545-207
17	758	24.7	484	1	US-08-111-939-12
18	616	20.1	458	3	US-09-233-989-9
19	609	19.8	438	1	US-08-111-939-17
20	609	19.8	641	3	US-09-233-989-10
21	582.5	19.0	454	3	US-09-233-989-4
22	576	18.8	476	3	US-09-233-989-3
23	574	18.7	476	3	US-09-233-989-2
24	574	18.7	476	4	US-09-917-254-67
25	572	18.6	476	3	US-09-233-989-6
26	565.5	18.4	435	1	US-08-111-939-14
27	564.5	18.4	435	1	US-08-111-939-16

28	564.5	18.4	435	1	US-08-452-262-2	Sequence 2, Appli
29	564.5	18.4	435	1	US-08-734-550-2	Sequence 2, Appli
30	564.5	18.4	435	5	PCT-US96-07528-2	Sequence 2, Appli
31	562.5	18.3	434	1	US-08-111-939-13	Sequence 13, Appli
32	562.5	18.3	434	3	US-09-233-989-7	Sequence 7, Appli
33	562.5	18.3	435	1	US-08-111-939-15	Sequence 15, Appli
34	487.5	15.9	561	3	US-09-233-989-5	Sequence 5, Appli
35	402.5	13.1	439	3	US-09-233-989-8	Sequence 8, Appli
36	402.5	13.1	443	4	US-09-976-594-527	Sequence 527, App
37	381.5	12.4	372	2	US-08-683-262B-64	Sequence 64, Appli
38	381.5	12.4	372	3	US-09-361-707-64	Sequence 64, Appli
39	282	9.2	109	1	US-08-111-939-19	Sequence 19, Appli
40	254	8.3	320	2	US-08-480-229C-20	Sequence 20, Appli
41	254	8.3	320	2	US-08-659-235C-20	Sequence 20, Appli
42	252.5	8.2	217	1	US-07-607-538C-3	Sequence 3, Appli
43	252.5	8.2	217	2	US-08-162-402B-3	Sequence 3, Appli
44	252.5	8.2	217	4	US-09-364-185-3	Sequence 3, Appli
45	252.5	8.2	218	1	US-07-607-538C-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-641-741-2  
; Sequence 2, Application US/09641741  
; Patent No. 6420155  
; GENERAL INFORMATION:  
; APPLICANT: Kerry E. Quinn  
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids  
; TITLE OF INVENTION: encoding Same  
; FILE REFERENCE: 15966-581  
; CURRENT APPLICATION NUMBER: US/09/641,741  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/159,613  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/224,086  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-641-741-2

Query Match	97.1%	Score 2980;	DB 4;	Length 734;
Best Local Similarity	78.2%	Pred. No. 8.5e-277;	Mismatches 0;	Indels 160; Gaps 1;
Matches 574;	Conservative 0;			
Qy	1	MWGLLLAALFAFAVGPALGAPNSVLGAPQGTTKVPGSTPALHSSPAQPPAETANGTS	60	
Db	1	MWGLLLAALFAFAVGPALGAPNSVLGAPQGTTKVPGSTPALHSSPAQPPAETANGTS	60	
Qy	61	EQHVRIRVIKKKVIKKRKKLTTRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL	120	
Db	61	EQHVRIRVIKKKVIKKRKKLTTRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL	120	
Qy	121	ESLRVSDSRLEASSSSQSGFLGPHRGRLNTQSGLEDGLYDGAWCAEQDADPMFQVDAGH	180	
Db	121	ESLRVSDSRLEASSSSQSGFLGPHRGRLNTQSGLEDGLYDGAWCAEQDADPMFQVDAGH	180	
Qy	181	PTRFSGVITQGRNSVMRYDWVTYSYKQVFSNDRSTWGRNSHSSGMDAVFPANSDPETPVL	240	
Db	181	PTRFSGVITQGRNSVMRYDWVTYSYKQVFSNDRSTWGRNSHSSGMDAVFPANSDPETPVL	240	
Qy	241	NLLPEQVAFRIRLLPQTWLOGGAPCLRAILACPVSDDPNDLFLAPASSSSDPLDFQHH	300	
Db	241	NLLPEQVAFRIRLLPQTWLOGGAPCLRAILACPVSDDPNDLFLAPASSSSDPLDFQHH	300	



; PRIOR FILING DATE: 1996-08-30  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-650-284B-2

Query Match 96.9%; Score 2976; DB 4; Length 734;  
Best Local Similarity 78.18; Pred. No. 2.1e-276;  
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

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QY 1 MWGILLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
DB 1 MWGILLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EOHVRIRVIKKKVIKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEQGTGCPPLGL 120
DB 61 EOHVRIRVIKKKVIKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEQGTGCPPLGL 120
QY 121 ESLRVSRSLEASSQSFGLGPHRGRINI QSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
DB 121 ESLRVSRSLEASSQSFGLGPHRGRINI QSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
QY 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
DB 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
QY 241 NLPEPQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDFQHH 300
DB 241 NLPEPQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDFQHH 300
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
DB 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
QY 361 GNEALGRELLLLMQFLCHEFRLGNPRVTRLLSEMR IHLLPSMNPDCGYEYAYHRGSELVG 420
DB 361 GNEALGRELLLLMQFLCHEFRLGNPRVTRLLSEMR IHLLPSMNPDCGYEYAYHRGSELVG 420
QY 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVP HVPNHHLP LPTVYTL PNAIVAPETR 480
DB 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVP HVPNHHLP LPTVYTL PNAIVAPETR 480
QY 481 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 509
DB 481 AVIKWMKRIPFVLSANLHGGLVVSYPFDTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
QY 510 ----- 509
DB 541 LAMQDTSRRPCHSQDPSVHGNIINGADWHTVPGSMNDFS YLHTNCFEVTVELSCDKPPHE 600
QY 510 ----- 509
DB 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGADIADAVIAGDINHDTVATWAGGDY 660
QY 510 ----- -MYTASAEYHSTVTRNCRTVTFEEGPPCNFVLT KTKPQKRLRELLAAGAKVPP 560
DB 661 WRLLTPGDYVMTASAEYHSTVTRNCRTVTFEEGPPCNFVLT KTKPQKRLRELLAAGAKVPP 720
QY 561 DLRRRLERLRGQKD 574
DB 721 DLRRRLERLRGQKD 734
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RESULT 4  
US-09-641-741-32  
; Sequence 32, Application US/09641741  
; Patent No. 6420155  
; GENERAL INFORMATION:  
; APPLICANT: Kerry E. Quinn  
; APPLICANT: CuraGen Corporation

; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids  
; TITLE OF INVENTION: encoding Same  
; FILE REFERENCES: 15966-581  
; CURRENT APPLICATION NUMBER: US/09/641,741  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/159,613  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/224,086  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 722  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-641-741-32

Query Match 77.5%; Score 2378.5; DB 4; Length 722;  
Best Local Similarity 64.3%; Pred. No. 4.4e-219;  
Matches 471; Conservative 34; Mismatches 57; Indels 171; Gaps 5;

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QY 1 MWGILLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
DB 1 MWGILLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EOHVRIRVIKKKVIKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEQGTGCPPLGL 120
DB 53 ERHVRIRVIKKKVIKKRKK--LRHPGLCTGTRPVVTHPAKTLTLPEKQEGCPCPLGL 110
QY 121 ESLRVSRSLEASSQSFGLGPHRGRINI QSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
DB 111 ESLRVSRSLEASSQSFGLGPHRGRINI QSGLEDGLYDGAWCAEQDADPMFQVDAGH 170
QY 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
DB 171 PVRFAGIVTQGRNSVMRYDWVTSYKQVFSNDSRTWKS RN-STGMDIVFPANSDAETPVL 229
QY 241 NLPEPQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDFQHH 300
DB 230 NLPEPQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLEAHTLGSSSLDFRHH 289
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
DB 290 NYKAMRKLKMQVNEQCPNITRIYSIGSHOGLKLYVMEMSDHFGHEHGEPEVRYVAGMH 349
QY 361 GNEALGRELLLLMQFLCHEFRLGNPRVTRLLSEMR IHLLPSMNPDCGYEYAYHRGSELVG 420
DB 350 GNEALGRELLLLMQFLCHEFRLGDPVTRLLTETRIHLLPSMNPDCGYEYAYHRGSELVG 409
QY 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVP HVPNHHLP LPTVYTL PNAIVAPETR 480
DB 410 WAEGRWTHQSIDLNHNFPADLNTQMTAEADDGLVPDTPVNHHLPLPTVYTL PNAIVAPETW 469
QY 481 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 510
DB 470 AVIKWMKRIPFVLSANLHGGLVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGTN 529
QY 511 ----- 510
DB 530 RAMQDTSRRPCHSQDPSLHGNVINGADWHTVPGSMNDFS YLHTNCFEVTVELSCDKPPHE 589
QY 511 ----- 510
DB 590 KELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGADIADAVIAGDINHDTVATWAGGDY 649
QY 511 ----- -VTASAEYHSTVTRNCRTVTFEEGPPCNFVLT KTKPQKRLRELLAAGAKVPP 560
DB 650 WRLLTPGDYVMTASAEYHSTVTRNCRTVTFEEGPPCNFVLT KTKPQKRLRELLAAGAKVPP 709
QY 561 DLRRRLERLRGQK 573
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Db 710 DLRKLERLRGQK 722

RESULT 5  
US-09-641-741-31  
; Sequence 31, Application US/09641741  
; Patent No. 6420155  
; GENERAL INFORMATION:  
; APPLICANT: Kerry E. Quinn  
; APPLICANT: Curagen Corporation  
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids  
; TITLE OF INVENTION: encoding Same  
; FILE REFERENCE: 45966-581  
; CURRENT APPLICATION NUMBER: US/09/641,741  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/159,613  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/224,086  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-641-741-31

Query Match 45.6%; Score 1398.5; DB 4; Length 764;  
Best Local Similarity 39.4%; Pred. No. 5.5e-125;  
Matches 301; Conservative 79; Mismatches 176; Indels 207; Gaps 0;

QY 4 LLLAALAFAPAV-----GALGAP-----RNSVLGLAQPQGTGKVPSTPALH--- 4  
Db 11 LALLALVALAGVRAQGAFFEDYDSQELWRGRYGGHPEP-SPPELFSFMSHEDL 6  
QY 46 ---SSPAQPPAETANGTSEQHVIRVKKKVMKKRKKLTLTRPTP----- 8  
Db 70 RVBEQEQEHPQOCHRTPK-----KAIPKKA--PKREKLVAETPPGPKNSRKRGRSKN 1 2  
QY 90 LVTAGPLVTPTAGTLDPAKQBTGCPPLGLESRLVSDSRLEASSQSFGLGPHGRGLNI 1 9  
Db 123 LEKAASDDHGVVAHEDVRE-----SCPLGLETLKITDFOLHASTSKRYGLGAHGRGLNI 1 8  
QY 150 QSGLEDGDLYDGAWCAEQADPWFQDAGHPTRFSGVITQGRNSVMRYDWTYSYKVQFS 2 9  
Db 179 QAGINENDFYDGAWCAGRNDLHQWIEVDARLTKFTGVITQGRNSLWLSDWYTSYKVMVS 2 8  
QY 210 NDSRTWGRNSHSGMDVFPANSDPETVNLNLLPEPQVAFIRLLPQWLOGGAPCLRA 2 9  
Db 239 NDSHTWTVKNGSG--DMIFEGNSEKEIPVNLPEPVMVARYIRINPQSFNDSICMRM 2 6  
QY 270 EILACPVSNDPLFLAPASGSDPLDFQHNHYKAMKMLKQVQECNPITRIYSIGKSY 3 9  
Db 297 EILGCLPDPNNYHRRNEMTTTDDDFKHNYKEMRQLMKVNMCPNITRIYNIKSH 3 6  
QY 330 QGLKLYMEMSDKPGHELGEPVRYAGMHGNEALGRELLLLLOFLCHEFLRGNPVT 3 9  
Db 357 QGLKLYAVSISDHPGHEVGEPEFHYIAGAHGNEVLGRELLLLHFLCQEYSAQNARIV 4 5  
QY 390 RLLSEMRHLLPSMNPDPGEIAYHRGSELVGAEGRWNNQSIDLNHNFDALNTPLWEAQD 4 3  
Db 417 RLVEETRIIHLPSLNDPGEKAYEGSELGWSLGRTHWDGIDINNFPDLNLSLWEAED 4 5  
QY 450 DGKVPVHPVNHLLPLFTYTLNATVAPETRAVIKMKRIPVLSANLHGGSELVSYSPFD 5 3  
Db 477 QQNAPRKVPNNHYIAIPFWLSENAATVATRAVIAMKEIPFVLGNLQGGSELVVAYPD 5 5  
QY 510 M----- 5 3  
Db 537 MVRSLMKTEHTTTPDDHVRFLAYSASTHRLMTDARRRVCHTDFQKEGTNGASWH 5 5

QY 511 ----- 510

Db 597 TVAGSLNDSYLHNCNFELSIYVGCDCYPHESELPEWENNRESLIVFMQVHRGKIGIV 656

QY 511 -----VTASAEQYHSVTRNCRVTFE 530

Db 657 RDLQKGISNAVISVEGVNHDIRTASDGDYWRLLNPGVYVVTAKAEGFITSTKNCMVGYD 716

QY 531 EGFPPCNFVLTPTKORRELLAAGAKVPPDPLRRRLERLRGQK 573

Db 717 MGATRCDFTLTKTNLARIREIMETFGQKQVSLPSRRLKLRGK 759

RESULT 6  
US-10-140-002-392  
; Sequence 392, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: ACIDS ENCODING THE SAME  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 392  
; LENGTH: 756  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-002-392

Query Match 45.3%; Score 1390.5; DB 4; Length 756;  
Best Local Similarity 40.0%; Pred. No. 3.2e-124;  
Matches 299; Conservative 76; Mismatches 185; Indels 187; Gaps 8;

QY 4 LLLAALAFAPAVGAPALGAP-----RNSVLGLAQPQGTGKVPSTPALHSSPAQSPAE 54  
Db 15 LLAVTLAGVGAQGALEDDPYGQEIWSRPEFYARPEP---ELETFSPPL---PAGPGE 68  
QY 55 TANGTSEQHVIRVIRVKKKVMKKRKKLTLTRPTPLVLTAGPLVTPPT---PAGTLDPA-- 108  
Db 69 WERRPQEPRPKPKATPKKA--PKREKSAPEPPPPGKHNSKVMRTKSSKAANDHSHVR 126  
QY 109 ---EKQBTGCPPLGLESRLVSDSRLEASSQSFGLGPHGRGLNIQSGLEDGDLYDGAWCA 165  
Db 127 VAREDVRESCPPLGLETLKITDFOLHASTVKRYGLGAHGRGLNIQAGINENDFYDGAWCA 186  
QY 166 EQQADPWFQDAGHPTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGRNSHSGM 225  
Db 187 GRNDLQWIEVDARLTRFTGVITQGRNSLWLSDWYTSYKVMVSNDSHTWTVKNGSG-- 244  
QY 226 DAVFPANSDPETVNLNLLPEPQVAFIRLLPQWLOGGAPCLRAEILACPVSPNDPLFLE 285  
Db 245 DMIFEGNSEKEIPVNLPEPVMVARYIRINPQSFNDSICMRMEILGCLPLPDPNNYHR 304  
QY 286 APASGSDPLDFQHNHYKAMKMLKQVQECNPITRIYSIGKSYQGLKLYMEMSDKPG 345

Db 305 RNEMTTDDLLDFKHNYKEMRQLMKVNMCPNITRIYNIQSHQGLKLYAVEISDRHPE 364  
Qy 346 HELGEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLISEMIRHLLPSNWP 405  
Db 365 HEVGEPEPHYTAGAGHNEVLGRELLLLLVQVCQEYLARNARIVHLVEETRIHVLPSLNP 424  
Qy 406 DGYEIAHYRGSSELVGAEGRWNNOSIDLNNHNFADLNTPLWEAODDGKVPHPVPHHLP 465  
Db 425 DGYEKAYEGGSELGWSLGRWTHDIDINNNFPDLNTLLWEAEDRQNVKPVNHYAIP 484  
Qy 466 TTYTLPNATVAPETRAVTKMKRIPFVLSANLHGELVVSPPFM 510  
Db 485 EWFLSENATVAAETRAVIAWMEKIPFVLGGNLOGGELVWAYPYDLVRSPKMQEHTPTPD 544  
Qy 511 ----- 510  
Db 545 DHVFRWLAYSASTHRLMTDARRVCHTEDFOKEEGTVNGASWITVAGSLNDFSYLHTNC 604  
Qy 511 ----- 510  
Db 605 FELSIYVCDKYPHESQLPEWENNRESLIVFMQVHRGIKGLYRDSHGKGI PNALISVE 664  
Qy 511 -----VTASAEHYHVSUTRNCRTVTFEGPPPCNFVLTTPKQ 546  
Db 665 GINHDIRTANDGDYWRLLNPGYYVVTAKAEGFTASTKNCVMGYDMGATRCDFTLSTNMA 724  
Qy 547 RLRELLAAGAKVPPDLRRRLRLRGOK 573  
Db 725 RIREIMEKFGQPVSLPARLKLGRK 751

## RESULT 7

US-08-111-939-2  
; Sequence 2, Application US/08111939  
; Patent No. 5460951  
; GENERAL INFORMATION:  
; APPLICANT: Kawai, Shinji  
; APPLICANT: Takeshita, Sunao  
; APPLICANT: Okazaki, Makoto  
; APPLICANT: Amann, Egon  
; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like  
; TITLE OF INVENTION: Protein and Process for its Production  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/111,939  
; FILING DATE: 26-AUG-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 324033/92  
; FILING DATE: 03-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 230029/92  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 33,694  
; REFERENCE/DOCKET NUMBER: 02481.1321-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-111-939-2

Query Match 38.5%; Score 1180.5; DB 1; Length 1128;  
Best Local Similarity 37.8%; Pred. No. 8.5e-104;  
Matches 246; Conservative 75; Mismatches 134; Indels 195; Gaps 6;

Qy 107 PABKQETGCPPLGLESRLVSDSRLEASSQSFGILGPHRGRLNIQSGLDEGLDYDGAWCAE 166  
Db 370 PVEKIK--CPPIGWESHRIEDNQIRASSMLRHGLGAQRGLNMQAGANEDDYDGAWCAE 427  
Qy 167 EQADAPWFQVADGHPTRFSGVITQGRNSVWRVYDWTYSKYQFQNSDSTWGRNSRHSGMD 226  
Db 428 DESQTQWIEVDTRTTRFTGVTITQGRDSSIHDDFVTTFVFGFSNDSQTWMTNGYEEM- 486  
Qy 227 AVFPANSDPETPVNLNLLPEQVAFRFLLPQTLQGCAPCLRAEILACPVSDPNDLPLEA 286  
Db 487 -TFYGNVDKDTPLVSELPEPVVARFRIYPLTW--NGSLCMRLEVLGCPVTPVYSYAQN 543  
Qy 287 PASGSSDPLDFQHNHYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMMSDKPGEH 346  
Db 544 EVV-TTDSLDFRHSYKDMQLMKANVEECPITRIYSLGKSSGLKIYAMEISDNFGDH 602  
Qy 347 ELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 406  
Db 603 ELGEPEFRYTAGIHGNEVLGRELLLLLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 662  
Qy 407 GYEIAHYRGSSELVGAEGRWNNOSIDLNNHNFADLNTPLWEAODDGKVPHPVPHHLP 466  
Db 663 GYEIAHYRGSSELVGAEGRWNNOSIDLNNHNFADLNTPLWEAODDGKVPHPVPHHLP 722  
Qy 467 YVTLPNATVAPETRAVTKMKRIPFVLSANLHGELVVSPPFM 510  
Db 723 RYLSPDATVSTEVRALISWMEKNPFVLGNLNGERLVSYDWMARTPSOEQLLAALAA 782  
Qy 511 ----- 510  
Db 783 ARGEDDDGVSEAQETPDHAFIRMLAIFASAHLTMTPEYRGCGQAQDYTSGMGIVNGAKW 842  
Qy 511 ----- 510  
Db 843 NPSRGTFNDFSYLHTNCLLSVYLGCDFKPFHESELPREWENNKBALTFMEQVHRGIKGV 902  
Qy 511 -----VTASAEHYHVSUTRNCRTVTF 529  
Db 903 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEVRTAHAEGYTSSAKICNDVY 962  
Qy 530 EGGFFPCNFVLTTPKORLRELLAAGAKVP-----PDLRRRLER 568  
Db 963 DIGATQCNFILARNKRIREILLAMNGRPILGVDPSRPMTPOORRMOOR 1012

## RESULT 8

US-09-641-741-30  
; Sequence 30, Application US/09641741  
; Patent No. 6420155  
; GENERAL INFORMATION:  
; APPLICANT: Kerry E. Quinn  
; APPLICANT: CuraGen Corporation  
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids  
; TITLE OF INVENTION: encoding Same  
; FILE REFERENCE: 15966-581  
; CURRENT APPLICATION NUMBER: US/09/641,741  
; CURRENT FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/159,613  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534

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; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 30
; LENGTH: 1128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-741-30

Query Match
Best Local Similarity 38.5%; Score 1180.5; DB 4; Length 1128;
Matches 246; Conservative 75; Mismatches 134; Indels 195; Gaps 6;

QY 107 PAEKQETGCPPLGLESURVSDSRLEASSQSFGLPGRRLNIQSGLDGLYDGAACAE 16
DB 370 PVEKIK--CPPIGMESHRIEDNOIRASSMLRHGLGAQRGLNMQAGANEDDYDGAACAE 47
QY 167 EQADAPWFQVDAGHTFSGVITQGRNSVMRYDWVTSYKQVFNDSRTWMSRHHSSGMD 26
DB 428 DESQTMIEVDTRTTRFTGTGTQGRDSSIHDDFVTFVGFNSDSTQVMYTYNGEEM- 46
QY 227 AVFPANSDPETPVNLNLLPEPQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLEA 26
DB 487 -TFYGNVDKDTPELSELPEPVAARFIYPLTW--NGSLCMRLEVLCGPVTPVYSYQAQ 53
QY 287 PASGSDPLDFOHNYKAMRKLKMQVOBQCPNITRIYSIGKSYQGLKLYVMEMSKPGEH 36
DB 544 EVV--TTDSLDFRHSYKDMRQMKAVNEECPTITRTYSLGKSRGLKIYAMEISDNPGDH 62
QY 347 ELGEPEVRYVAGMHNAGRELLLLMQFLCHEFLRGNPRVTRLLSEMRIHLPLSMNPD 46
DB 603 ELGEPEFRYTAGIHGNEVLGRELLLLMQFLCQYRDGNPRVRLVQDTRIHLVPSLND 62
QY 407 GYETIHRGSELVAGMAGRNWNSQIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPT 46
DB 663 GYEVAAQMGSEFGNWLGLTEGDFIDFDPDLNSVLWAAEKKWVPYRVVNNLPIE 72
QY 467 YITLPNATVAPETRAVIKMKRIPFVLSANLHGELVVSYPFDM-----50
DB 723 RYLSPDATVSTEVRALIIISWMEKNPFVLGNLNGERLVSYPYDMARTPSQQLAEALAA 72
QY 511 -----50
DB 783 ARGEDDDGVSEAQETPDHAIFRWLAIASFASAHLTMTPEYRGCGQAQDYTSGMGIVNGAKW 82
QY 511 -----50
DB 843 NPRSGTFNDFSYLHTNCLLSVYLGCDKPFHESELPREWENKKEALLTFMEQVHRIGKV 92
QY 511 -----VTASAGYHSVTRNCRVTF 59
DB 903 VTDEQGIPIANATISVSGINHGVTASGGDYWRILNPGEYRVTAHAEGYTSSAKICNVDY 92
QY 530 EGGPFCNFVLTKPKORRELLAAGAKVP-----PDLRRRLER 568
DB 963 DIGATQCNFILARSNWKRIREILAMNGNRPILGVDPSPRMTPOQRMMQOR 1012

RESULT 9
US-09-060-482-8
; Sequence 8, Application US/09060482
; Patent No. 6468766
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Layne, Matthew D.
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE
; FILE REFERENCE: 05433/036001
; CURRENT APPLICATION NUMBER: US/09/060,482
; CURRENT FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 08/18,009
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: US 60/013,439
; EARLIER FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 1128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-060-482-8

Query Match
Best Local Similarity 37.8%; Pred. No. 8.5e-104;
Matches 246; Conservative 75; Mismatches 134; Indels 195; Gaps 6;

QY 107 PAEKQETGCPPLGLESURVSDSRLEASSQSFGLPGRRLNIQSGLDGLYDGAACAE 166
DB 370 PVEKIK--CPPIGMESHRIEDNOIRASSMLRHGLGAQRGLNMQAGANEDDYDGAACAE 427
QY 167 EQADAPWFQVDAGHTFSGVITQGRNSVMRYDWVTSYKQVFNDSRTWMSRHHSSGMD 226
DB 428 DESQTMIEVDTRTTRFTGTGTQGRDSSIHDDFVTFVGFNSDSTQVMYTYNGEEM- 486
QY 227 AVFPANSDPETPVNLNLLPEPQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLEA 286
DB 487 -TFYGNVDKDTPELSELPEPVAARFIYPLTW--NGSLCMRLEVLCGPVTPVYSYQAQ 543
QY 287 PASGSDPLDFOHNYKAMRKLKMQVOBQCPNITRIYSIGKSYQGLKLYVMEMSKPGEH 346
DB 544 EVV--TTDSLDFRHSYKDMRQMKAVNEECPTITRTYSLGKSRGLKIYAMEISDNPGDH 602
QY 347 ELGEPEVRYVAGMHNAGRELLLLMQFLCHEFLRGNPRVTRLLSEMRIHLPLSMNPD 406
DB 603 ELGEPEFRYTAGIHGNEVLGRELLLLMQFLCQYRDGNPRVRLVQDTRIHLVPSLND 662
QY 407 GYETIHRGSELVAGMAGRNWNSQIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPT 466
DB 663 GYEVAAQMGSEFGNWLGLTEGDFIDFDPDLNSVLWAAEKKWVPYRVVNNLPIE 722
QY 467 YITLPNATVAPETRAVIKMKRIPFVLSANLHGELVVSYPFDM-----510
DB 723 RYLSPDATVSTEVRALIIISWMEKNPFVLGNLNGERLVSYPYDMARTPSQQLAEALAA 782
QY 511 -----510
DB 783 ARGEDDDGVSEAQETPDHAIFRWLAIASFASAHLTMTPEYRGCGQAQDYTSGMGIVNGAKW 842
QY 511 -----510
DB 843 NPRSGTFNDFSYLHTNCLLSVYLGCDKPFHESELPREWENKKEALLTFMEQVHRIGKV 902
QY 511 -----VTASAGYHSVTRNCRVTF 529
DB 903 VTDEQGIPIANATISVSGINHGVTASGGDYWRILNPGEYRVTAHAEGYTSSAKICNVDY 962
QY 530 EGGPFCNFVLTKPKORRELLAAGAKVP-----PDLRRRLER 568
DB 963 DIGATQCNFILARSNWKRIREILAMNGNRPILGVDPSPRMTPOQRMMQOR 1012

RESULT 10
US-09-641-741-29
; Sequence 29, Application US/09641741
; Patent No. 6420155
; GENERAL INFORMATION:
; APPLICANT: Kerry E. Quinn
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; FILE REFERENCE: encoding Same
; FILE REFERENCE: 15966-581
; CURRENT APPLICATION NUMBER: US/09/641,741
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613

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; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/224,086  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 29  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-641-741-29

Query Match 38.0%; Score 1166; DB 4; Length 845;  
Best Local Similarity 37.7%; Pred. No. 1.3e-102;  
Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8;

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QY 107 PAEKQETGCPPLGLESIRVSDSRLEASSQSFGLGPHRGRLNQTOSGLEDDGLYDGAWCAE 166
DB 66 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRGLNMQTGATEDDDYDGAWCAE 123
QY 167 EQADAPWFQVDAGHPTFRFSGVITQGRNSVMRYDWTYSYKQVQFNSDRTWNGSRNHSSGMD 226
DB 124 DDARTQWIEVDTRTRFTGVTQGRDSSIHDFVITFFVGFNSDSTQWMTYNGYEEM- 182
QY 227 AVFPANSDPETPVNLNLLPEQVAFIRLLPQTWLGQAPCLRAEILACPVSDPNDLFLEA 286
DB 183 -TFHGNVDKQTPVLSPELPVAFIRIYPLTW--NGSLCWRLEVLGCSVAPVYSYAQN 239
QY 287 PASGSDPLDFQHHNYKAMKLMQVQEQCPNTRIYSIGSKYQGLKLYWEMSDKPGEH 346
DB 240 EVV-ATDLDLFRHSHYKDMRQMLKVNEECPTTIRIYSLGKSRGLKIYAMEISDNGEH 298
QY 347 ELGEPEVRYVAGMHGNEALGRELILLMQFLCHFLRGNPRVTRLLSEMIHLLPSMNP 406
DB 299 ELGEPEFRYTAGIHGNEVLGRELILLMQFLCHFLRGNPRVTRLLSEMIHLLPSMNP 358
QY 407 GYBIAHRGSELVGMWAEGRWNQSIDLNHNFADLNTPLWEAQDDGKVPHTVPNNHLLPLPT 466
DB 359 GYEVAQMGSFPGNWALGLWTEEGDFIDFDPDLSVLMGAEERKWPVYRVPNNLPIPE 418
QY 467 YYTLPNATVAPETRAVIKWKMRIPFVLSANLHGELVVSYPFDM----- 510
DB 419 RYLSPDATVSTEVRAIIAMWKNPFFVLGANGELRVSYPYDMARTPTQELLAAAMAA 478
QY 511 ----- 510
DB 479 ARGEDEDEVSEAQETPDHAIFRWLAISFASAHLLTLEPYRGCGQAQDYTGGMGIVNGAKW 538
QY 511 ----- 510
DB 539 NPRTGTINDPSYLHNTCLELSFYLGCDFPHESELPREWENKEALLTFMEQVHRGIGKV 598
QY 511 -----VTASAGYHSTVTRNCRVTF 529
DB 599 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNV 658
QY 530 EGGPEPCNFVLTTPKQRLRELLAAGAKVP-----PDLR---RLRG 571
DB 659 DIGATQCNFILARSNWKRIREIMAMNGNRPPIPHIDPSRPMTPQOORLQORLQRLRLRA 718
QY 572 Q 572
DB 719 Q 719
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## RESULT 11

US-09-060-482-2  
; Sequence 2, Application US/09060482  
; Patent No. 6468766  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Mu-En  
; APPLICANT: Layne, Matthew D.

; APPLICANT: Yet, Shaw-Fang  
; TITLE OF INVENTION: AORTIC CARDIOXYPEPTIDASE-LIKE POLYPEPTIDE  
; FILE REFERENCE: 05433/036001  
; CURRENT APPLICATION NUMBER: US/09/060,482  
; CURRENT FILING DATE: 1998-04-15  
; EARLIER APPLICATION NUMBER: US 081818,009  
; EARLIER FILING DATE: 1997-03-14  
; EARLIER APPLICATION NUMBER: US 601013,439  
; EARLIER FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-060-482-2

Query Match 38.0%; Score 1166; DB 4; Length 1158;  
Best Local Similarity 37.7%; Pred. No. 2.2e-102;  
Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8;

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QY 107 PAEKQETGCPPLGLESIRVSDSRLEASSQSFGLGPHRGRLNQTOSGLEDDGLYDGAWCAE 166
DB 379 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRGLNMQTGATEDDDYDGAWCAE 436
QY 167 EQADAPWFQVDAGHPTFRFSGVITQGRNSVMRYDWTYSYKQVQFNSDRTWNGSRNHSSGMD 226
DB 437 DDARTQWIEVDTRTRFTGVTQGRDSSIHDFVITFFVGFNSDSTQWMTYNGYEEM- 495
QY 227 AVFPANSDPETPVNLNLLPEQVAFIRLLPQTWLGQAPCLRAEILACPVSDPNDLFLEA 286
DB 496 -TFHGNVDKQTPVLSPELPVAFIRIYPLTW--NGSLCWRLEVLGCSVAPVYSYAQN 552
QY 287 PASGSDPLDFQHHNYKAMKLMQVQEQCPNTRIYSIGSKYQGLKLYWEMSDKPGEH 346
DB 553 EVV-ATDLDLFRHSHYKDMRQMLKVNEECPTTIRIYSLGKSRGLKIYAMEISDNGEH 611
QY 347 ELGEPEVRYVAGMHGNEALGRELILLMQFLCHFLRGNPRVTRLLSEMIHLLPSMNP 406
DB 612 ELGEPEFRYTAGIHGNEVLGRELILLMQFLCHFLRGNPRVTRLLSEMIHLLPSMNP 671
QY 407 GYBIAHRGSELVGMWAEGRWNQSIDLNHNFADLNTPLWEAQDDGKVPHTVPNNHLLPLPT 466
DB 672 GYEVAQMGSFPGNWALGLWTEEGDFIDFDPDLSVLMGAEERKWPVYRVPNNLPIPE 731
QY 467 YYTLPNATVAPETRAVIKWKMRIPFVLSANLHGELVVSYPFDM----- 510
DB 732 RYLSPDATVSTEVRAIIAMWKNPFFVLGANGELRVSYPYDMARTPTQELLAAAMAA 791
QY 511 ----- 510
DB 792 ARGEDEDEVSEAQETPDHAIFRWLAISFASAHLLTLEPYRGCGQAQDYTGGMGIVNGAKW 851
QY 511 ----- 510
DB 852 NPRTGTINDPSYLHNTCLELSFYLGCDFPHESELPREWENKEALLTFMEQVHRGIGKV 911
QY 511 -----VTASAGYHSTVTRNCRVTF 529
DB 912 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNV 971
QY 530 EGGPEPCNFVLTTPKQRLRELLAAGAKVP-----PDLR---RLRG 571
DB 972 DIGATQCNFILARSNWKRIREIMAMNGNRPPIPHIDPSRPMTPQOORLQORLQRLRLRA 1031
QY 572 Q 572
DB 1032 Q 1032
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## RESULT 12

US-09-148-545-140  
; Sequence 140, Application US/09148545

Patent No. 6590075  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 70 Human Secreted Proteins  
FILE REFERENCE: P2001P  
CURRENT APPLICATION NUMBER: US/09/148,545  
CURRENT FILING DATE: 1998-09-04  
EARLIER APPLICATION NUMBER: PCT/US98/04482  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,161  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
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EARLIER APPLICATION NUMBER: 60/043,671  
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EARLIER APPLICATION NUMBER: 60/043,674  
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EARLIER APPLICATION NUMBER: 60/043,672  
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EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,878  
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EARLIER APPLICATION NUMBER: 60/056,882  
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EARLIER APPLICATION NUMBER: 60/056,637  
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EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
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EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056,636  
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EARLIER APPLICATION NUMBER: 60/056,874  
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EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 05-Sep-1997  
EARLIER APPLICATION NUMBER: 60/047,599





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QY 511 -----V : 1
Db 476 KEALLTFMEQVHRGIGVTVDEGIPANATISVSGINHGVTASGQDYWRILNPGEYRV : 15
QY 512 TASAEGYHSVTRNCRVTFEGPPFCNFVLTKPKQRLRELLAAGAKVP -----P : 10
Db 536 TAAEGYTSAKICNDYDIGATQCNCNFILARSNWKIRBEILAMNGRPFILRVDPSRPMTF : 15
QY 561 DLRRRLER 568
Db 596 QRRMQOR 603

RESULT 14
US-09-370-838-34
; Sequence 34, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSTICS OF
; LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-34

Query Match 32.7%; Score 1002.5; DB 4; Length 506;
Best Local Similarity 39.9%; Pred. No. 2.9e-87;
Matches 200; Conservative 51; Mismatches 91; Indels 159; Gaps 1;

QY 232 NSDPETPVNLNLPPEQVAFIRLLPQTLWLOGGAPCLRAEILACPVSDPNDLFLEAPASGS 2 1
Db 1 NSEKEIPVLNELPVPVARYIRINPQSWFDNGSICMRMEILGCLPDPNNYHRRNEMTT 6
QY 292 SDPLDFQHHNYKAMRKLKMQVQEOCPNITRIYSIGKSYQGLKLYVMEMSKPGEHELGE 3 1
Db 61 TDDLDFKHHNYKEMRQMKVVMCMCNITRIYNGKSHQGLKLYAVEISDHPGEHEVGE 1 0
QY 352 EYRVAGMGNEALGRELLLLMQFLCHFEFLRGNPVTRLLSEMRHLLPSMNPDPGYEIA 4 1
Db 121 EFHYIAGAHGNEVLGRELLLLHFLCQYSQAQNAIRVRLVEETRIHILPSLNPDPGYE 1 0
QY 412 YHRGSELVGMAGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHLLPLPTYYTLP 4 1
Db 181 YEGGSELGWSLGRWTHDGDIDNNFPDLNLLWEAEDQQAQNAIRVRLVEETRIHILPS 2 0
QY 472 NATVAPETRAVIKWKMRIPFVLSANLHGELVVSYPFDM----- 5 0
Db 241 NATVATETRAVIAMWEKIPFVLGNLQGGELVVAIPYDMVRSRLWKTQEHPTTPDDHV 3 0
QY 511 ----- 5 0
Db 301 LAYSASTHRLMTDARRVCHTEDFQKEBGTVNGASWHTVAGSLNDFSYLHTNCFELSI 3 0
QY 511 ----- 5 0
Db 361 VCCDKYPHESELPEWENNRESLIVFMEQVHRGIGIVRDLQGGKIGISNAVISVEGVNHI 4 0
QY 511 -----VTASAEGYHSVTRNCRVTFEGPPFCNFVLTKPKQRLRELL 5 2
```

```
Db 421 RTASDGDYWRLLNPGEYVVTAKAEGFITSTKNCMVGYDMGATRCDFTLTKTLNLAIREIM 480
QY 553 AAGAKVPDPDLRRRLERLRGQK 573
Db 481 ETFGQPVSLPSRRLKLRGK 501

RESULT 15
US-09-854-133-34
; Sequence 34, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-34

Query Match 32.7%; Score 1002.5; DB 4; Length 506;
Best Local Similarity 39.9%; Pred. No. 2.9e-87;
Matches 200; Conservative 51; Mismatches 91; Indels 159; Gaps 1;

QY 232 NSDPETPVNLNLPPEQVAFIRLLPQTLWLOGGAPCLRAEILACPVSDPNDLFLEAPASGS 291
Db 1 NSEKEIPVLNELPVPVARYIRINPQSWFDNGSICMRMEILGCLPDPNNYHRRNEMTT 60
QY 292 SDPLDFQHHNYKAMRKLKMQVQEOCPNITRIYSIGKSYQGLKLYVMEMSKPGEHELGE 351
Db 61 TDDLDFKHHNYKEMRQMKVVMCMCNITRIYNGKSHQGLKLYAVEISDHPGEHEVGE 120
QY 352 EYRVAGMGNEALGRELLLLMQFLCHFEFLRGNPVTRLLSEMRHLLPSMNPDPGYEIA 411
Db 121 EFHYIAGAHGNEVLGRELLLLHFLCQYSQAQNAIRVRLVEETRIHILPSLNPDPGYE 180
QY 412 YHRGSELVGMAGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHLLPLPTYYTLP 471
Db 181 YEGGSELGWSLGRWTHDGDIDNNFPDLNLLWEAEDQQAQNAIRVRLVEETRIHILPS 240
QY 472 NATVAPETRAVIKWKMRIPFVLSANLHGELVVSYPFDM----- 510
Db 241 NATVATETRAVIAMWEKIPFVLGNLQGGELVVAIPYDMVRSRLWKTQEHPTTPDDHV 300
QY 511 ----- 510
Db 301 LAYSASTHRLMTDARRVCHTEDFQKEBGTVNGASWHTVAGSLNDFSYLHTNCFELSI 360
QY 511 ----- 510
Db 361 VCCDKYPHESELPEWENNRESLIVFMEQVHRGIGIVRDLQGGKIGISNAVISVEGVNHI 420
QY 511 -----VTASAEGYHSVTRNCRVTFEGPPFCNFVLTKPKQRLRELL 552
Db 421 RTASDGDYWRLLNPGEYVVTAKAEGFITSTKNCMVGYDMGATRCDFTLTKTLNLAIREIM 480
QY 553 AAGAKVPDPDLRRRLERLRGQK 573
Db 481 ETFGQPVSLPSRRLKLRGK 501
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Search completed: January 10, 2005, 19:39:06

Job time : 54 secs

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· his Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 19:19:34 ; Search time 154 Seconds  
(without alignments)  
1337.082 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLLAALAPAVGALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3070	100.0	574	7 ADC71542	Adc71542 Human NOV
2	3070	100.0	574	8 ADN33953	Adn33953 Human nov
3	3070	100.0	574	8 ADO42303	Ado42303 Human NOV
4	2980	97.1	734	4 AAB47184	Aab47184 ACPLX pro
5	2980	97.1	734	4 AAG65917	Aag65917 Amino aci
6	2980	97.1	734	7 ADC71546	Adc71546 Human NOV
7	2980	97.1	734	7 ADC71540	Adc71540 Human NOV
8	2980	97.1	734	7 ADP65320	Adp65320 Human met
9	2980	97.1	734	8 ADN33957	Adn33957 Human nov
10	2980	97.1	734	8 ADO42301	Ado42301 Human NOV
11	2980	97.1	734	8 ADO42305	Ado42305 Human NOV
12	2980	97.1	734	8 ADO42307	Ado42307 Human NOV
13	2976	96.9	734	4 AAB36174	Aab36174 Human APG
14	2976	96.9	734	7 ADJ63969	Adj63969 Human PRO
15	2975	96.9	734	4 AAU29252	Aau29252 Human APG
16	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
17	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
18	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
19	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
20	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
21	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
22	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
23	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
24	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
25	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO

ALIGNMENTS

RESULT 1

ADC71542

ID ADC71542 standard; protein; 574 AA.

XX ADC71542;

DT 18-DEC-2003 (first entry)

XX Human NOV7b protein SEQ ID NO:170.

human; NOV; cytostatic; anorectic; antidiabetic; antiparkinsonian;  
neuroprotective; nootropic; immunomodulator; antiarteriosclerotic;  
nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;  
diabetes; metabolic disorder; anorexia; neurodegenerative disease;  
Parkinson's disease; Alzheimer's disease; immune disorder;  
haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;  
hypoglycaemia; bone disorder; wasting disorder.

XX Homo sapiens.

XX WO2003040329-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035535.

XX 05-NOV-2001; 2001US-0338626P.

XX 28-NOV-2001; 2001US-00996015.

XX 28-NOV-2001; 2001US-033912P.

XX 03-DEC-2001; 2001US-0334300P.

XX 19-APR-2002; 2002US-0373806P.

XX 16-MAY-2002; 2002US-0381043P.

XX 07-AUG-2002; 2002US-0401593P.

XX 04-NOV-2002; 2002US-00287190.

(CURA-) CURAGEN CORP.

Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;  
Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangoli EA;  
Gerlach VL, Guo X, Ji W, Khramtsov NV, Leite MW, Li L, Mezes PG;  
Millet I, Ooi CE, Ort T, Padigara M, Patturajan M, Pena CE;  
Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;  
Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;  
Zhong M;  
WPI; 2003-441554/41.  
N-PSDB; ADC71541.

Abu92788 Human sec  
Abo08865 Human sec  
Abo02917 Human sec  
Abr75071 Human sec  
Abr94833 Human sec  
Abu85806 Human PRO  
Abu98966 Novel hum  
Abu98181 Novel hum  
Abu91887 Novel hum  
Abu89580 Human PRO  
Abu84421 Human sec  
Abu67634 Human sec  
Abu80662 Human PRO  
Abr99580 Human sec  
Abr99970 Human sec  
Abo16493 Human sec  
Abr92393 Human sec  
Abo19034 Human sec  
Abr78455 Human sec  
Abu85191 Novel hum



PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;  
PI Gerlach V, Guo XS, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;  
PI Millet I, Ooi CE, Ort T, Padigar M, Patturajan M, Pena CA;  
PI Rastelli L, Rieger DK, Senger KEQ, Smithson G, Spaderna SK;  
PI Szytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;  
PI Zhong M;  
XX  
DR WPI; 2004-213932/20.  
DR N-PSDB; ADN33952.  
XX  
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.  
XX  
PS Claim 2; SEQ ID NO 170; 129pp; English.

CC The invention relates to 87 isolated NOVX polypeptides (NOV1-NOV5), their  
CC mature forms and their encoding polynucleotides having sequence  
CC similarity to pancreatic polypeptide (NOV1), angiotensin (NOV2),  
CC interleukin-1 (NOV3), endothelin-2 (NOV4), endozepine (NOV5),  
CC amphiregulin (NOV6) and metalloproteinase (NOV7). Also included the  
CC use of NOVX in the manufacture of a medicament for treating a human  
CC disease associated with NOVX, detecting NOVX in a sample via an  
CC immunoassay, identifying an agent that binds to the NOVX polypeptide,  
CC modulating the activity of NOVX, a vector comprising NOVX polynucleotide,  
CC a cell comprising the vector, an antibody that immunospecifically binds  
CC to NOVX, detecting the polynucleotide in a sample using a hybridisation  
CC assay; and producing the polypeptide comprising culturing the cell under  
CC conditions that lead to expression of the polypeptide. NOVX and its  
CC polynucleotide are used to prevent, diagnose or treat a medical condition  
CC in human related to the aberrant expression and activity of NOVX  
CC polypeptides e.g. metabolic disorders, diabetes, obesity, infectious  
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative  
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. NOVX may also be used as  
CC an antigen in the production of antibodies and in assays to identify  
CC modulators (agonists and antagonists) of the expression and activity of  
CC NOVX. The present sequence represents a NOVX protein.

XX  
SQ Sequence 574 AA;

Query Match 100.0%; Score 3070; DB 8; Length 574;  
Best Local Similarity 100.0%; Pred. No. 2.3e-277;  
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLLLAALAPAVGAPALCAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
DB 1 MWGLLLAALAPAVGAPALCAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EQHVRIRVKKKVIKKRKKLTITRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120  
DB 61 EQHVRIRVKKKVIKKRKKLTITRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120  
QY 121 ESLRVSRLSEASSQSGFLGPHGRNLINISQGLDGLYDGCACAEQDADPWFQVDAGH 180  
DB 121 ESLRVSRLSEASSQSGFLGPHGRNLINISQGLDGLYDGCACAEQDADPWFQVDAGH 180  
QY 181 PTFSGVITGCRNSVMRYDWTYSKYQFSDNRSTWGRNSHSSGMDAVFPANSDPETPVL 240  
DB 181 PTFSGVITGCRNSVMRYDWTYSKYQFSDNRSTWGRNSHSSGMDAVFPANSDPETPVL 240  
QY 241 NLPEPQVAFIRLLPTWLGAGAPLCAETILACPVSDPNDLFLFAPASGSDPLDPQHH 300  
DB 241 NLPEPQVAFIRLLPTWLGAGAPLCAETILACPVSDPNDLFLFAPASGSDPLDPQHH 300  
QY 301 NYKAMRKLKMQVQOCNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
DB 301 NYKAMRKLKMQVQOCNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
QY 361 GNPALGRELLELLLMQFICHEFLRGNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRSGLVG 420  
DB 361 GNPALGRELLELLLMQFICHEFLRGNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRSGLVG 420

Db 361 GNPALGRELLELLLMQFICHEFLRGNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRSGLVG 420  
QY 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPPIHVPNHHLLPLPTYYTTLPNATVAPETR 480  
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPPIHVPNHHLLPLPTYYTTLPNATVAPETR 480  
QY 481 AVIKWMKRIPIFVLISANLHGGLVVSYPFDMVTASAEGYHSVTRNCRVTFEGPPPCNFVL 540  
Db 481 AVIKWMKRIPIFVLISANLHGGLVVSYPFDMVTASAEGYHSVTRNCRVTFEGPPPCNFVL 540  
QY 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574  
Db 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

RESULT 3

AD042303  
ID AD042303 standard; protein; 574 AA.

XX  
AC AD042303;

DT 15-JUL-2004 (first entry)

XX Human NOVX polypeptide #76.

DE Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;  
KW Parkinson's disease; graft-versus-host disease; scleroderma;  
KW hypertension; haemophilia; idiopathic thrombocytopenic purpura;  
KW immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease;  
KW bronchial asthma; anorexia; cancer-associated cachexia;  
KW multiple sclerosis; fertility.

XX Homo sapiens.

XX US2004059338-A1.

XX 25-MAR-2004.

XX 02-DEC-2002; 2002US-00307817.

XX 03-DEC-2001; 2001US-0336881P.

XX 05-DEC-2001; 2001US-0336820P.

XX 07-DEC-2001; 2001US-0338285P.

XX 10-DEC-2001; 2001US-0338318P.

XX 10-DEC-2001; 2001US-0338989P.

XX 11-DEC-2001; 2001US-0339022P.

XX 11-DEC-2001; 2001US-0339314P.

XX 11-DEC-2001; 2001US-0339516P.

XX 11-DEC-2001; 2001US-0339517P.

XX 12-DEC-2001; 2001US-0339611P.

XX 12-DEC-2001; 2001US-0340981P.

XX 12-DEC-2001; 2001US-0341346P.

XX 14-DEC-2001; 2001US-0340390P.

XX 14-DEC-2001; 2001US-0340440P.

XX 14-DEC-2001; 2001US-0340565P.

XX 14-DEC-2001; 2001US-0340608P.

XX 17-DEC-2001; 2001US-0341144P.

XX 17-DEC-2001; 2001US-0341477P.

XX 17-DEC-2001; 2001US-0341540P.

XX 18-DEC-2001; 2001US-0341768P.

XX 20-DEC-2001; 2001US-0342592P.

XX 31-DEC-2001; 2001US-0344903P.

XX 01-FEB-2002; 2002US-0353286P.

XX 01-FEB-2002; 2002US-0353288P.

XX 26-FEB-2002; 2002US-0359599P.

XX 26-FEB-2002; 2002US-0359626P.

XX 26-FEB-2002; 2002US-0359671P.

XX 27-FEB-2002; 2002US-0359914P.

XX 27-FEB-2002; 2002US-0359956P.

XX 28-FEB-2002; 2002US-0360924P.

XX 28-FEB-2002; 2002US-0360964P.

XX 28-FEB-2002; 2002US-0361028P.

XX 28-FEB-2002; 2002US-0361256P.

PR	28-FEB-2002;	2002US-0361264P.	PI	Padigar M, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PR	05-MAR-2002;	2002US-0361770P.	PI	Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
PR	13-MAR-2002;	2002US-0362230P.	PI	Stone DU, Taupier RU, Vernet CAM, Voss EZ, Zhong M;
PR	13-MAR-2002;	2002US-0364181P.	XX	WPI; 2004-268786/25.
PR	15-MAR-2002;	2002US-0364238P.	DR	N-PSDB; ADO42302.
PR	15-MAR-2002;	2002US-0364978P.	XX	
PR	17-APR-2002;	2002US-0373288P.	XX	
PR	15-MAY-2002;	2002US-0373288P.	XX	
PR	15-MAY-2002;	2002US-0380981P.	PT	New human NOVX polypeptides and nucleic acid molecules, useful for
PR	16-MAY-2002;	2002US-0381004P.	PT	diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
PR	17-MAY-2002;	2002US-0381495P.	PT	atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PR	28-MAY-2002;	2002US-0383534P.	XX	scleroderma.
PR	28-MAY-2002;	2002US-0383744P.	PS	Claim 1; SEQ ID NO 152; 610pp; English.
PR	29-MAY-2002;	2002US-0383829P.	XX	
PR	29-MAY-2002;	2002US-0384024P.	XX	
PR	02-JUL-2002;	2002US-0393332P.	CC	The invention relates to human NOVX polypeptides and the polynucleotides
PR	06-AUG-2002;	2002US-0401315P.	CC	encoding them. The invention also relates to antibodies specific to the
PR	07-AUG-2002;	2002US-0401788P.	CC	NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
PR	20-AUG-2002;	2002US-0401788P.	CC	useful for manufacturing a medicament for treating a syndrome associated
PR	23-AUG-2002;	2002US-0405400P.	CC	with a human disease, such as a pathology associated with the NOVX
PR	23-AUG-2002;	2002US-0405400P.	CC	polypeptide. The sequences are useful for diagnosing, treating or
PR	23-AUG-2002;	2002US-0405684P.	CC	preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
PR	23-AUG-2002;	2002US-0405684P.	CC	diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
PR	23-AUG-2002;	2002US-0405687P.	CC	disease, scleroderma, immunodeficiencies, AIDS, dyslipidemia,
PR	23-AUG-2002;	2002US-0405698P.	CC	thrombocytopenic purpura, bronchial asthma, anorexia, cancer-associated
PR	26-AUG-2002;	2002US-0406353P.	CC	obesity, Crohn's disease, hypertension, haemophilia, idiopathic
XX	(AGEE//)	AGEE M L.	CC	cachexia, multiple sclerosis or fertility. The nucleic acids may be used
PA	(ALSO//)	ALSOBROOK J P.	CC	as hybridisation probes, in chromosome mapping, in tissue typing, in
PA	(ANDE//)	ANDERSON D W.	CC	preventive medicine or in pharmacogenomics. This sequence represents a
PA	(BERG//)	BERGHS C.	CC	human NOVX polypeptide of the invention.
PA	(BOLD//)	BOLDG F L.	XX	Sequence 574 AA;
PA	(BURG//)	BURGESS C E.	QY	Query Match
PA	(CATT//)	CATTERTON E.	Db	Best Local Similarity 100.0%; Score 3070; DB 8; Length 574;
PA	(DIPI//)	DIPIPPO V A.	QY	Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PA	(EDIN//)	EDINGER S R.	Db	1 MWGLLLAALAPAPAVGALGAPNSVLGLAQPGTGTGKVPSTPALHSSPAQPAETANGTS 60
PA	(EISE//)	EISEN A.	QY	1 MWGLLLAALAPAPAVGALGAPNSVLGLAQPGTGTGKVPSTPALHSSPAQPAETANGTS 60
PA	(ELLE//)	ELLERMAN K.	Db	61 EQHVRIRIVIKKKVIMKKRKLTLTRETPLVLTAGPLVTPAGTLDPAEKQETGCPPLGL 120
PA	(GANG//)	GANGOLLI E A.	Db	61 EQHVRIRIVIKKKVIMKKRKLTLTRETPLVLTAGPLVTPAGTLDPAEKQETGCPPLGL 120
PA	(GERL//)	GERLACH V.	QY	121 ESLRVSLSLEASSSSQSGFLGPHRGRNLIOGLEDGLDYGAWCAEQDADPWQVDAGH 180
PA	(GORM//)	GORMAN L.	Db	121 ESLRVSLSLEASSSSQSGFLGPHRGRNLIOGLEDGLDYGAWCAEQDADPWQVDAGH 180
PA	(ROTH//)	ROTHBERG B G.	QY	181 PTRPSGVITQGRNSVMRYDWTYSKYQFNSDRTWMSRNSHSSGMDAVFPANSDPETPVL 240
PA	(HERR//)	HERMANN J L.	Db	181 PTRPSGVITQGRNSVMRYDWTYSKYQFNSDRTWMSRNSHSSGMDAVFPANSDPETPVL 240
PA	(HALV//)	HALVORSEN Y.	QY	241 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACVSDPNLDFLEAPASGSDPLDFQHH 300
PA	(JIMW//)	JIM W.	Db	241 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACVSDPNLDFLEAPASGSDPLDFQHH 300
PA	(KEKU//)	KEKUDA R.	QY	301 NYXAMRKLKMQVQEQCPNITRIYSIGSKYQGLKLYVMEMSDKPEHELGEPVRYVAGMH 360
PA	(KHRA//)	KHRAMTSOV N V.	Db	301 NYXAMRKLKMQVQEQCPNITRIYSIGSKYQGLKLYVMEMSDKPEHELGEPVRYVAGMH 360
PA	(LARO//)	LAROCHELLE W J.	QY	361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLISEMIHLLPSMNPQGYEIAVHRGSELVG 420
PA	(LEPL//)	LEPLEY D M.	Db	361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLISEMIHLLPSMNPQGYEIAVHRGSELVG 420
PA	(LILL//)	LI L.	QY	421 WAEGRWNNQSIDLNHNFDADNTPLWEAQDDGKVPVHVPNNHLLPLTYTYTLPLNATVAPETR 480
PA	(MACD//)	MACDOUGALL J R.	Db	421 WAEGRWNNQSIDLNHNFDADNTPLWEAQDDGKVPVHVPNNHLLPLTYTYTLPLNATVAPETR 480
PA	(MILL//)	MILLER C E.	QY	481 AVIKWMKRIPFVLISANLHGELVSYFFDMVTASAEYHSVTRNCRVTFEEGPFPCNFVL 540
PA	(ORTT//)	ORT T.	Db	481 AVIKWMKRIPFVLISANLHGELVSYFFDMVTASAEYHSVTRNCRVTFEEGPFPCNFVL 540
PA	(PADI//)	PADIGARU M.	QY	541 TKTPKORLELLAAGAKAVPPDLRRRLRLRGQKD 574
PA	(PATT//)	PATTURAJAN M.	PI	Agee ML, Alsobrook JP, Anderson DW, Barghs C, Boldog FL;
PA	(PENY//)	PENYMAN J A.	PI	Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
PA	(RIEG//)	RIEGER D K.	PI	Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG,
PA	(ROTH//)	ROTHENBERG M E.	PI	Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;
PA	(SHEN//)	SHENOY S G.	PI	Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE,
PA	(SMIT//)	SMITHSON G.	PI	Ort T;
PA	(SPAD//)	SPADERNA S K.	PI	
PA	(SPYT//)	SPYTEK K A.	PI	
PA	(STON//)	STONE D J.	PI	
PA	(TAUP//)	TAUPIER R J.	PI	
PA	(VERN//)	VERNET C A M.	PI	
PA	(VOSS//)	VOSS E Z.	PI	
PA	(ZHON//)	ZHONG M.	PI	





PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;  
PI Lai Y;  
XX WPI; 2001-632223/73.  
DR N-PSDB; AA167207.  
XX Isolated polypeptides, which may be peptide hormones, which are  
PT identified by high throughput genome-based biology which identifies genes  
PT and gene products as therapeutic targets for treatment of diseases such  
PT as diabetes and cancer.  
XX Claim 1; Page 97-98; 99pp; English.  
XX The invention provides polypeptides (AAG65886-65918) which may be peptide  
CC hormones (including insulin, growth hormones, chemokines, cytokines,  
CC neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic  
CC hormones, neuropepsin, pituitary hormones, pleiotrophins, prostaglandin,  
CC secretogranins, selectins, thromboglobulins, thymosins) identified by  
CC high throughput genome-based biology and polynucleotides (AA167196-67201)  
CC encoding them. The polypeptides can be expressed by standard recombinant  
CC methodology. The polypeptides are useful in the treatment of disease such  
CC as diabetes, breast-, prostate-, colon cancer and other malignant tumor,  
CC hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities,  
CC asthma, manic depression, dementia, delirium, mental retardation,  
CC Huntington's disease, Tourette's syndrome, schizophrenia, alcoholism, mental  
CC or sexual development disorders, and dysfunctions of the blood cascade  
CC system including those leading to stroke. The polynucleotides may be used  
CC as diagnostic reagents through detecting mutations in the associated gene  
CC and for chromosome localization and for tissue expression studies. The  
CC polypeptides and polynucleotides may also be used as vaccines  
XX Sequence 734 AA;  
SQ Query Match 97.1%; Score 2980; DB 4; Length 734;  
Best Local Similarity 78.2%; Pred. No. 9e-269; 0; Mismatches 160; Gaps 1;  
Matches 574; Conservative 0; Indels 160; Gaps 1;  
QY 1 MWGLLLAALAFAPAVGALCAPNSVLGAQPTTKVQSTPAHSSPAQPAFTANGTS 6  
DB 1 MWGLLLAALAFAPAVGALCAPNSVLGAQPTTKVQSTPAHSSPAQPAFTANGTS 6  
QY 61 EQHVRIRVKKKVIKKRKLTLTPTPLVTAAGPLVTPAGTLDPAEQETGCPPLGL 1 0  
DB 61 EQHVRIRVKKKVIKKRKLTLTPTPLVTAAGPLVTPAGTLDPAEQETGCPPLGL 1 0  
QY 121 ESLRVSLSLEASSQSFGLPGRHRLNTOGLEDGLYDGAWCABEQDADPWFQVDAGH 1 0  
DB 121 ESLRVSLSLEASSQSFGLPGRHRLNTOGLEDGLYDGAWCABEQDADPWFQVDAGH 1 0  
QY 181 PTFSGVITQGRNSVVRDYDVTYSKYQFNSDSTWGSNHSNGMDVFPANSDDETPVL 2 0  
DB 181 PTFSGVITQGRNSVVRDYDVTYSKYQFNSDSTWGSNHSNGMDVFPANSDDETPVL 2 0  
QY 241 NLLPEQVAFRILLPQTLQGGAPCLRAEILACPVSDNDLFLAPASGSDPLDFQHH 3 0  
DB 241 NLLPEQVAFRILLPQTLQGGAPCLRAEILACPVSDNDLFLAPASGSDPLDFQHH 3 0  
QY 301 NYKAMEKLMKQVQCPNITRYSYKQYGLKLYMENSDFGHELGEPVRYVAGMH 3 0  
DB 301 NYKAMEKLMKQVQCPNITRYSYKQYGLKLYMENSDFGHELGEPVRYVAGMH 3 0  
QY 361 GNEALGRELILLMOPLCHEFTLRGNPRVTRLLSEMRHLLPSMNDPGYEIAYHRSSELVG 4 0  
DB 361 GNEALGRELILLMOPLCHEFTLRGNPRVTRLLSEMRHLLPSMNDPGYEIAYHRSSELVG 4 0  
QY 421 WAEGRWNNOSIDNNFADNLTPLWEAQDQKGVPHIVNNHLLPLTYTTLNATVAPETR 4 0  
DB 421 WAEGRWNNOSIDNNFADNLTPLWEAQDQKGVPHIVNNHLLPLTYTTLNATVAPETR 4 0  
QY 481 AVIKWKRIPTFVLSANLGGELVSVYDPTD----- 50  
DB 481 AVIKWKRIPTFVLSANLGGELVSVYDPTDTPWAARELTFTPDPAVRLWSTVYAGSN 54

QY 510 ----- 509  
DB 541 LAMQDTSRRPCHSQDPSVHGNIINGADMHTVPGSMNDFSYLHNCFEVTVLSCKDFPHE 600  
QY 510 ----- 509  
DB 601 NELPQWENNKDALLTYLEQVRMGIAGVVRDKDTBELGIADAVIAVDGINHDVTTAWGGDY 660  
QY 510 -----MYTASAGVHSVTRNCRVTFEFGFFPCNFVLTPTKPKORLRELLAAGAKVPP 560  
DB 661 WRLLTPGDYMWVTASAGVHSVTRNCRVTFEFGFFPCNFVLTPTKPKORLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGXKD 574  
DB 721 DLRRRLRLRGXKD 734  
RESULT 6  
ID ADC71546  
XX ADC71546 standard; protein; 734 AA.  
AC ADC71546;  
XX 18-DEC-2003 (first entry)  
DE Human NOV7d protein SEQ ID NO:174.  
XX human; NOVX; cytostatic; anorectic; antidiabetic; antiparkinsonian;  
KW neuroprotective; nootropic; immunomodulator; antiarteriosclerotic;  
KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;  
KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; immune disorder;  
KW haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;  
KW hypoglycaemia; bone disorder; wasting disorder.  
XX Homo sapiens.  
XX WO2003040329-A2.  
XX 15-MAY-2003.  
XX 05-NOV-2002; 2002WO-US035535.  
XX 05-NOV-2001; 2001US-0338626P.  
XX 28-NOV-2001; 2001US-00996015.  
XX 28-NOV-2001; 2001US-033912P.  
XX 29-NOV-2001; 2001US-0334300P.  
XX 03-DEC-2001; 2001US-0338196P.  
XX 19-APR-2002; 2002US-0373806P.  
XX 16-MAY-2002; 2002US-0381043P.  
XX 07-AUG-2002; 2002US-0401593P.  
XX 04-NOV-2002; 2002US-00287190.  
XX (CURA-) CURAGEN CORP.  
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;  
XX Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;  
XX Gerlach VL, Guo X, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;  
XX Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CE;  
XX Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;  
XX Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;  
XX Zhong M;  
XX WPI; 2003-441554/41.  
XX N-PSDB; ADC71545.  
XX New NOVX polypeptides and nucleic acids for diagnosing, preventing or  
XX treating NOVX-associated disorders, e.g. cancer, obesity, diabetes or  
XX atherosclerosis, and for chromosome mapping, tissue typing or  
XX pharmacogenomics.  
XX Claim 1; SEQ ID NO 174; 112pp; English.

CC The present invention describes novel human proteins designated NOVX,  
CC where X can be an integer of 1 to 7. The NOVX protein and nucleotide  
CC sequences have cytotatic, anorectic, antidiabetic, antiparkinsonian,  
CC neuroprotective, nootropic, immunomodulator, antiarteriosclerotic,  
CC nephrotropic and osteopathic activities, and can be used in vaccines and  
CC in gene therapy. The NOVX proteins can be used in manufacturing a  
CC medicament for treating a syndrome associated with a human disease, the  
CC disease selected from a pathology associated with the protein. The  
CC disease can be cancer. NOVX proteins, nucleic acid molecules and  
CC antibodies may also be used for diagnosing, treating or preventing other  
CC pathologies associated with aberrant NOVX expression or activity, such as  
CC obesity, diabetes, metabolic disorders, anorexia, neurodegenerative  
CC diseases (e.g. Parkinson's disease or Alzheimer's disease), immune  
CC disorders, haematopoietic disorders, atherosclerosis, renal failure,  
CC hyperkalaemia, hypoglycaemia, bone disorders and wasting disorders. The  
CC NOVX nucleic acids and proteins may also be used in chromosome mapping,  
CC tissue typing, predictive medicine and pharmacogenomics. The present  
CC sequence is used in the exemplification of the present invention. N.B.  
CC The present sequence is designated SEQ ID NO:174, but does not correspond  
CC with the sequence of SEQ ID NO:174 given on page 179.  
XX  
SQ Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;  
Best Local Similarity 78.2%; Pred. No. 9e-269;  
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGLLLALAPAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
DB 1 MWGLLLALAPAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPAGTLDPAEKQETCCPPLGL 120  
DB 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPAGTLDPAEKQETCCPPLGL 120  
QY 121 ESLRVSRSLEASSQSQFGLPHGRNLINQSGLEDGLYGCWCAERQDADPWFQVDAGH 180  
DB 121 ESLRVSRSLEASSQSQFGLPHGRNLINQSGLEDGLYGCWCAERQDADPWFQVDAGH 180  
QY 181 PTFSGVITGCRNSVRYDWVTSYKQVPSNDSRTWGRNSHSSGMDAVFPANSDPETPVL 240  
DB 181 PTFSGVITGCRNSVRYDWVTSYKQVPSNDSRTWGRNSHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPOTLQGGAPCLRAELACFVSDPNDLFLFAPASGSDPLDFQHH 300  
DB 241 NLLPEQVAFIRLLPOTLQGGAPCLRAELACFVSDPNDLFLFAPASGSDPLDFQHH 300  
QY 301 NYKAMRKLKQVQBCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGLGPEVRYVAGMH 360  
DB 301 NYKAMRKLKQVQBCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGLGPEVRYVAGMH 360  
QY 361 GNEALGRELILLMOFLCHSFLRGNPRVTRILLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
DB 361 GNEALGRELILLMOFLCHSFLRGNPRVTRILLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDQKGVPHIVPNHHLPLPTYTYTLPNATVAPETR 480  
DB 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDQKGVPHIVPNHHLPLPTYTYTLPNATVAPETR 480  
QY 481 AVIKWKRIPFVLISANLHGELVVSYPFD----- 509  
DB 481 AVIKWKRIPFVLISANLHGELVVSYPFDTRTPWAARELTPTDDAVFRWLSTVYAGSN 540  
QY 510 ----- 509  
DB 541 LAMQDTSRRRCHSQDSFVGHGNIINGADHMTVPGSMNDFSYLHNTCNFVTVELSCDKFPHE 600  
QY 510 ----- 509  
DB 601 NELPQEWNNKDALLTYLEQVRMGVAGVVRDKOTELGIADAVIADGINHDTVATWGGDY 660  
QY 510 -----MVTASAGYHSVTRNCRVTFEEGPPCNFVLTQKRLRELLAAGAKVPP 560  
|||||

DB 661 WRLITPGDYMVTASAGYHSVTRNCRVTFEEGPPCNFVLTQKRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
DB 721 DLRRRLRLRGQKD 734  
RESULT 7  
ID ADC71540 standard; protein; 734 AA.  
XX  
AC ADC71540;  
XX  
DT 18-DEC-2003 (first entry)  
DE Human NOV7a protein SEQ ID NO:168.  
XX  
KW human; NOVX; cytostatic; anorectic; antidiabetic; antiparkinsonian;  
KW neuroprotective; nootropic; immunomodulator; antiarteriosclerotic;  
KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;  
KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; immune disorder;  
KW haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;  
KW hypoglycaemia; bone disorder; wasting disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040329-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 05-NOV-2002; 2002WO-US035535.  
XX  
PR 05-NOV-2001; 2001US-0338626P.  
PR 28-NOV-2001; 2001US-00996015.  
PR 28-NOV-2001; 2001US-0333912P.  
PR 29-NOV-2001; 2001US-0334300P.  
PR 03-DEC-2001; 2001US-0338196P.  
PR 19-APR-2002; 2002US-0373806P.  
PR 16-MAY-2002; 2002US-0381043P.  
PR 07-AUG-2002; 2002US-0401593P.  
PR 04-NOV-2002; 2002US-00287190.  
XX  
(CURA-) CURAGEN CORP.  
PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;  
PI Chapoval A, Chaudhuri A, Binger SR, Eisen A, Gangolli EA;  
PI Gerlach VL, Guo X, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;  
PI Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CEA;  
PI Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;  
PI Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;  
PI Zhong M;  
DR WPI; 2003-441554/41.  
DR N-PSDB; ADC71539.  
XX  
XX New NOVX polypeptides and nucleic acids for diagnosing, preventing or  
PT treating NOVX-associated disorders, e.g. cancer, obesity, diabetes or  
PT atherosclerosis, and for chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Claim 1; SEQ ID NO 168; 112pp; English.  
XX  
CC The present invention describes novel human proteins designated NOVX,  
CC where X can be an integer of 1 to 7. The NOVX protein and nucleotide  
CC sequences have cytotatic, anorectic, antidiabetic, antiparkinsonian,  
CC neuroprotective, nootropic, immunomodulator, antiarteriosclerotic,  
CC nephrotropic and osteopathic activities, and can be used in vaccines and  
CC in gene therapy. The NOVX proteins can be used in manufacturing a  
CC medicament for treating a syndrome associated with a human disease, the  
CC disease selected from a pathology associated with the protein. The  
CC disease can be cancer. NOVX proteins, nucleic acid molecules and  
CC antibodies may also be used for diagnosing, treating or preventing other

CC pathologies associated with aberrant NOVX expression or activity, such as  
 CC obesity, diabetes, metabolic disorders, anorexia, neurodegenerative  
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease), immune  
 CC disorders, haematopoietic disorders, atherosclerosis, renal failure,  
 CC hyperkalaemia, hypoglycaemia, bone disorders and wasting disorders. The  
 CC NOVX nucleic acids and proteins may also be used in chromosome mapping,  
 CC tissue typing, predictive medicine and pharmacogenomics. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;  
 Best Local Similarity 78.2%; Pred. No. 9e-269;  
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
 QY 1 MWGILLALAAPAVGALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS ( )  
 DB 1 MWGILLALAAPAVGALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS ( )  
 QY 61 EOHVRIIVIKKVKIMKKRKLILTRTPDLVITAGPLVTPAGTLDPAEKQETGCPPLGL 1 10  
 DB 61 EOHVRIIVIKKVKIMKKRKLILTRTPDLVITAGPLVTPAGTLDPAEKQETGCPPLGL 1 10  
 QY 121 ESLVSDSRLEASSQSFGLGPHRGRNLIOGLEDGLYDGAWCABEQDADPFQVDAGH 1 10  
 DB 121 ESLVSDSRLEASSQSFGLGPHRGRNLIOGLEDGLYDGAWCABEQDADPFQVDAGH 1 10  
 QY 181 PTPSGVITGRNSVMRWYDWTYSYKQFSNDSRTWMSGRNHSMDAVFPANSDPTPYL 2 0  
 DB 181 PTPSGVITGRNSVMRWYDWTYSYKQFSNDSRTWMSGRNHSMDAVFPANSDPTPYL 2 0  
 QY 241 NLLPEPOAVPIRLLPOTWLOGGAPCLRAEILACPVSDNDPLFLEAPASGSDPLDFQHH 3 10  
 DB 241 NLLPEPOAVPIRLLPOTWLOGGAPCLRAEILACPVSDNDPLFLEAPASGSDPLDFQHH 3 10  
 QY 301 NYKAMRKLKMQVOECNPITRIYSIGKSYOGLKLYMEMSDKPEGHELGEPEVRYVAGMH 3 0  
 DB 301 NYKAMRKLKMQVOECNPITRIYSIGKSYOGLKLYMEMSDKPEGHELGEPEVRYVAGMH 3 0  
 QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMIHLLPSNMNPDGYEIAHRGSELVY 4 0  
 DB 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMIHLLPSNMNPDGYEIAHRGSELVY 4 0  
 QY 421 WAEGRNWNSIDLNHNPADLNTPLWBAQDDGKVPHTVPHNHLPLPTTYTLPNATVAPETR 4 0  
 DB 421 WAEGRNWNSIDLNHNPADLNTPLWBAQDDGKVPHTVPHNHLPLPTTYTLPNATVAPETR 4 0  
 QY 481 AVIKWMKRIPFVLSANLHGELVVSYPFD----- 5 9  
 DB 481 AVIKWMKRIPFVLSANLHGELVVSYPFD----- 5 9  
 QY 510 ----- 5 9  
 DB 510 ----- 5 9  
 QY 541 LAMQDTSRRPCHSQDFS VHNGIINGADWHTVFGSMNDFS YLHNTNCFEVTVELSCDKFPHE 6 0  
 DB 510 ----- 5 9  
 QY 601 NELPQWENNKDALLTYLEQVRMGIAGVVRDKDTELGIAADAVIADVGINHDVTTAWGGDY 6 0  
 QY 510 -----MYTASRGYHSVTRNCRVTFEEGPFPCNFVLTTPKQRLRELLAAGAKVPP 5 0  
 DB 661 WRLLTPGDMVTASRGYHSVTRNCRVTFEEGPFPCNFVLTTPKQRLRELLAAGAKVPP 7 0  
 QY 561 DLRRRLRLRGQKD 574  
 DB 721 DLRRRLRLRGQKD 734

RESULT 8  
 ADP65320  
 ID ADP65320 standard; protein; 734 AA.  
 XX  
 AC ADP65320;

XX DT 12-AUG-2004 (first entry)  
 DE Human metallocarboxypeptidase cpx-1.  
 XX  
 KW autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
 KW anarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; human.  
 XX  
 OS Homo sapiens.  
 XX WO2003072827-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 31-OCT-2002; 2002WO-US035433.  
 XX  
 PR 31-OCT-2001; 2001US-0336220P.  
 XX  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 PI Hirsch R, Thorton SL;  
 XX WPI; 2003-712740/67.  
 XX GENBANK; NP\_062555.  
 XX  
 PT Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 XX gout.  
 PS Disclosure; Page; 56pp; English.  
 CC  
 CC The invention relates to a novel method for diagnosing and analysing a  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises a treatment of rheumatoid arthritis. Identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This sequence represents a  
 CC protein sequence relating to the genes used in the analysis and treatment  
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown  
 CC in the specification. It has been supplied in an electronic format from  
 CC WIPO.  
 XX  
 SQ Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;  
 Best Local Similarity 78.2%; Pred. No. 9e-269;  
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
 QY 1 MWGILLALAAPAVGALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS 60  
 DB 1 MWGILLALAAPAVGALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS 60

QY 61 EQHVIRIVIKKKVIMKKRKKLTJTRPTPLVTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
D6 61 EQHVIRIVIKKKVIMKKRKKLTJTRPTPLVTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
QY 121 ESLRVSRLSEASSQSFGLPGRGRNIOGLEDGDLYDCAWCAEQDADPWQVDAGH 180  
D6 121 ESLRVSRLSEASSQSFGLPGRGRNIOGLEDGDLYDCAWCAEQDADPWQVDAGH 180  
QY 181 PTFESGVIQGRNSVRWYDWTYSKYQFSDNSRVTWGSNRHSSGMDAVFPANSDPETPVL 240  
D6 181 PTFESGVIQGRNSVRWYDWTYSKYQFSDNSRVTWGSNRHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVARIPLLPOTWLOGGAPCLRAETLACVSPDNDLFLFEPASGSSDPLDFQHH 300  
D6 241 NLLPEQVARIPLLPOTWLOGGAPCLRAETLACVSPDNDLFLFEPASGSSDPLDFQHH 300  
QY 301 NYKAWRKLKMOVQOCNITRIYSIGSKYQGLKLYVMEMSKPGEHELGPBEVRYVAGMH 360  
D6 301 NYKAWRKLKMOVQOCNITRIYSIGSKYQGLKLYVMEMSKPGEHELGPBEVRYVAGMH 360  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDPGYEYAYHRGSELVG 420  
D6 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDPGYEYAYHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHIIVPNHHLLPLPTYYTTLPNATVAPETR 480  
D6 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHIIVPNHHLLPLPTYYTTLPNATVAPETR 480  
QY 481 AVIKWKRIRIPVLSANLHGGELVVSYPFD----- 509  
D6 481 AVIKWKRIRIPVLSANLHGGELVVSYPFD----- 509  
QY 510 ----- 509  
D6 510 ----- 509  
QY 541 LAMQDTSRRPCHSQDSFVHGNIINGADHVTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600  
D6 510 ----- 509  
QY 601 NELPQEWENNKDALLTYLEQVRMGVGIAGVVRDKOTELGIADAVIADGGINHDVTTWAGGDY 660  
D6 510 -----MVTASAEYHSVTRNCRVTFEGPPPCNFVLTKTKPQRLRELLAAGAKVPP 560  
D6 661 WRLLTPGDYVMVTASAEYHSVTRNCRVTFEGPPPCNFVLTKTKPQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
D6 721 DLRRRLRLRGQKD 734  
RESULT 9  
ADN33957  
ID ADN33957 standard; protein; 734 AA.  
XX AC ADN33957;  
XX 17-JUN-2004 (first entry)  
XX DE Human novel protein NOV7d.  
XX KW Human; NOVX; pancreatic polypeptide; angiotensin; interleukin-1;  
KW endotoxin-2; endotoxin; amphiregulin; metalloproteinase;  
KW metabolic disorder; diabetes; obesity; infectious disease; anorexia;  
KW cancer; cancer-associated cachexia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidaemia; metabolic disturbance;  
KW metabolic syndrome X; wasting disorder; antibacterial agent.  
XX OS Homo sapiens.  
XX PN US2004038230-A1.  
XX 26-FEB-2004.  
XX

PF 04-NOV-2002; 2002US-00287190.  
XX 05-NOV-2001; 2001US-0338626P.  
PR 28-NOV-2001; 2001US-00996015.  
PR 28-NOV-2001; 2001US-0333912P.  
PR 29-NOV-2001; 2001US-0334300P.  
PR 03-DEC-2001; 2001US-0338196P.  
PR 19-APR-2002; 2002US-0373806P.  
PR 16-MAY-2002; 2002US-0381043P.  
PR 07-AUG-2002; 2002US-0401593P.  
XX (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CHAN/) CHANT J S.  
PA (CHAP/) CHAPOVAL A.  
PA (CHAU/) CHAUDHURI A.  
PA (EDIN/) EDINGER S R.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GUOX/) GUO X S.  
PA (JIWJ/) JI W.  
PA (KHRA/) KHRAMTSOV N V.  
PA (LEIT/) LEITE M W.  
PA (LILL/) LI L.  
PA (MEZE/) MEZES P S.  
PA (MILL/) MILLET I.  
PA (OOIC/) OOI C E.  
PA (ORTT/) ORT T.  
PA (PADI/) PADIGARU M.  
PA (PENA/) PENA C E A.  
PA (PAST/) PASTELLI L.  
PA (RIEG/) RIEGER D K.  
PA (SENG/) SENGHER K E Q.  
PA (SMIT/) SMITHSON G.  
PA (SPAD/) SPADERNA S K.  
PA (SPYT/) SPYTEK K A.  
PA (STON/) STONE D J.  
PA (TWOJ/) TWOMLOW N.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
PA (ZHON/) ZHONG M.  
XX  
PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;  
PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;  
PI Gerlach V, Guo XS, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;  
PI Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CE;  
PI Rastelli L, Rieger DK, Senger KEQ, Smithson G, Spaderna SK;  
PI Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zernhusen BD;  
PI Zhong M;  
XX WPI; 2004-213932/20.  
DR N-PSDB; ADN33956.  
XX  
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.  
XX  
XX Claim 2; SEQ ID NO 174; 129pp; English.  
XX  
CC The invention relates to 87 isolated NOVX polypeptides (NOV1-NOV5), their  
CC mature forms and their encoding polynucleotides having sequence  
CC similarity to pancreatic polypeptide (NOV1), angiotensin (NOV2),  
CC interleukin-1 (NOV3), endotoxin-2 (NOV4), endotoxin (NOV5),  
CC amphiregulin (NOV6) and metalloproteinase (NOV7). Also included the  
CC use of NOVX in the manufacture of a medicament for treating a human  
CC disease associated with NOVX, detecting NOVX in a sample via an  
CC immunoassay, identifying an agent that binds to the NOVX polypeptide,  
CC modulating the activity of NOVX, a vector comprising NOVX polynucleotide,  
CC a cell comprising the vector, an antibody that immunospecifically binds

CC to NOVX, detecting the polynucleotide in a sample using a hybridization  
CC assay; and producing the polypeptide comprising culturing the cell under  
CC conditions that lead to expression of the polypeptide NOVX and its und:  
CC polynucleotide are used to prevent, diagnose or treat a medical condition  
CC in human related to the aberrant expression and activity of NOVX  
CC polypeptides e.g. metabolic disorders, diabetes, obesity, infectious  
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative,  
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents NOVX may also be used as  
CC an antigen in the production of antibodies and in assays to identify  
CC modulators (agonists and antagonists) of the expression and activity of  
CC NOVX. The present sequence represents a NOVX protein.

XX Sequence 734 AA;

Query Match		97.1%; Score 2980; DB 8; Length 734;
Best Local Similarity		78.2%; Pred. No. 9e-269; 0; Mismatches 0; Indels 160; Gaps 1;
Matches 574; Conservative		
QY	1	MWGLLLAALAPAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSPAPPAETANGTS 6
DB	1	MWGLLLAALAPAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSPAPPAETANGTS 6
QY	61	BOHVRIRVKKKVIKKRKKLTITRPTPLVTAAGLVTPTAGTLDPAEKQETGCPPLGL 1 0
DB	61	EQHVRIRVKKKVIKKRKKLTITRPTPLVTAAGLVTPTAGTLDPAEKQETGCPPLGL 1 0
QY	121	ESLRVSDRLSEASSQSGFLGPHRGRLNTOSGLEGDLVDGAWCAEQADPWFQVDAGH 1 0
DB	121	ESLRVSDRLSEASSQSGFLGPHRGRLNTOSGLEGDLVDGAWCAEQADPWFQVDAGH 1 0
QY	181	PTPFSGVITOGNSVNRVYDWTYKYQFSNDSTWWSNRHSSGMDAVFPANSDPPTVYL 2 0
DB	181	PTPFSGVITOGNSVNRVYDWTYKYQFSNDSTWWSNRHSSGMDAVFPANSDPPTVYL 2 0
QY	241	NLIPPEQVAFIRLLPOTWLOGAPCLRAEILACPVSDNDPLFLEAPASGSDPLDFQHH 3 0
DB	241	NLIPPEQVAFIRLLPOTWLOGAPCLRAEILACPVSDNDPLFLEAPASGSDPLDFQHH 3 0
QY	301	NYKAMKLLMKQVQECFNTRIYSIGKSYQGLKLYVMSDKPGBHELGEPEVRVYAGMH 3 0
DB	301	NYKAMKLLMKQVQECFNTRIYSIGKSYQGLKLYVMSDKPGBHELGEPEVRVYAGMH 3 0
QY	361	GNELGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELVG 4 0
DB	361	GNELGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELVG 4 0
QY	421	WAEGRWNQSIDLNNFADNTPLWEAQDDGKVPPIVNNHLLPLPTTYTLNATVAPETR 4 0
DB	421	WAEGRWNQSIDLNNFADNTPLWEAQDDGKVPPIVNNHLLPLPTTYTLNATVAPETR 4 0
QY	481	AVIKWMKRIPFVLSANLHSGELVSYSPD----- 50
DB	481	AVIKWMKRIPFVLSANLHSGELVSYSPD----- 50
QY	510	----- 50
DB	510	----- 50
QY	541	LAMQDTSRPPCHSQDPSVHGNTINGADMHTVPGSMNDFSYLHNTCFEVTVELSCDKPFHE 60
DB	541	LAMQDTSRPPCHSQDPSVHGNTINGADMHTVPGSMNDFSYLHNTCFEVTVELSCDKPFHE 60
QY	510	----- 50
DB	510	----- 50
QY	601	NELPOEWENNKDALLTYLEQVRNAGVVRKOTELGIADAVIADGINHDVTTAWGGDY 66
DB	601	NELPOEWENNKDALLTYLEQVRNAGVVRKOTELGIADAVIADGINHDVTTAWGGDY 66
QY	510	----- 50
DB	510	----- 50
QY	661	WLLPTFGDVMVTASAEVHVSVRNCRVTFEEGPPFCNFVLTPTKQRLRELLAAGAKVPP 56
DB	661	WLLPTFGDVMVTASAEVHVSVRNCRVTFEEGPPFCNFVLTPTKQRLRELLAAGAKVPP 56
QY	561	DURRLERLRGQKD 574
DB	561	DURRLERLRGQKD 574
QY	721	DURRLERLRGQKD 734
DB	721	DURRLERLRGQKD 734

RESULT 10  
ADO42301

ID ADO42301 standard; protein; 734 AA.

XX ADO42301;

XX 15-JUL-2004 (first entry)

XX Human NOVX polypeptide #75.

XX Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;  
XX Parkinson's disease; graft-versus-host disease; scleroderma;  
XX immunotension; haemophilia; idiopathic thrombocytopenic purpura;  
XX immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease;  
XX bronchial asthma; anorexia; cancer-associated cachexia;  
XX multiple sclerosis; fertility.

XX Homo sapiens.

XX US2004058338-A1.

XX 25-MAR-2004.

XX 02-DEC-2002; 2002US-00307817.

XX 03-DEC-2001; 2001US-0336881P.

XX 05-DEC-2001; 2001US-0336820P.

XX 07-DEC-2001; 2001US-0338285P.

XX 10-DEC-2001; 2001US-0338318P.

XX 10-DEC-2001; 2001US-0338989P.

XX 11-DEC-2001; 2001US-0339022P.

XX 11-DEC-2001; 2001US-0339314P.

XX 11-DEC-2001; 2001US-0339516P.

XX 11-DEC-2001; 2001US-0339517P.

XX 12-DEC-2001; 2001US-0339611P.

XX 12-DEC-2001; 2001US-0340981P.

XX 12-DEC-2001; 2001US-0341346P.

XX 14-DEC-2001; 2001US-0340390P.

XX 14-DEC-2001; 2001US-0340440P.

XX 14-DEC-2001; 2001US-0340565P.

XX 14-DEC-2001; 2001US-0340608P.

XX 14-DEC-2001; 2001US-0341144P.

XX 17-DEC-2001; 2001US-0341477P.

XX 17-DEC-2001; 2001US-0341540P.

XX 18-DEC-2001; 2001US-0341768P.

XX 20-DEC-2001; 2001US-0342592P.

XX 31-DEC-2001; 2001US-0344903P.

XX 01-FEB-2002; 2002US-0353286P.

XX 01-FEB-2002; 2002US-0353288P.

XX 26-FEB-2002; 2002US-0359599P.

XX 26-FEB-2002; 2002US-0359626P.

XX 26-FEB-2002; 2002US-0359671P.

XX 27-FEB-2002; 2002US-0359914P.

XX 27-FEB-2002; 2002US-0359956P.

XX 28-FEB-2002; 2002US-0360924P.

XX 28-FEB-2002; 2002US-0360964P.

XX 28-FEB-2002; 2002US-0361028P.

XX 28-FEB-2002; 2002US-0361256P.

XX 28-FEB-2002; 2002US-0361264P.

XX 05-MAR-2002; 2002US-0361770P.

XX 05-MAR-2002; 2002US-0362230P.

XX 13-MAR-2002; 2002US-0364181P.

XX 13-MAR-2002; 2002US-0364238P.

XX 15-MAR-2002; 2002US-0364978P.

XX 17-MAR-2002; 2002US-0365025P.

XX 17-APR-2002; 2002US-0373288P.

XX 15-MAY-2002; 2002US-0380981P.

XX 17-MAY-2002; 2002US-0381004P.

XX 17-MAY-2002; 2002US-0381495P.

XX 28-MAY-2002; 2002US-0383534P.

XX 28-MAY-2002; 2002US-0383744P.

PR 29-MAY-2002; 2002US-0383829P.  
 PR 29-MAY-2002; 2002US-0384024P.  
 PR 02-JUL-2002; 2002US-0393332P.  
 PR 06-AUG-2002; 2002US-0401315P.  
 PR 07-AUG-2002; 2002US-0401788P.  
 PR 20-AUG-2002; 2002US-0404676P.  
 PR 23-AUG-2002; 2002US-0405400P.  
 PR 23-AUG-2002; 2002US-0405684P.  
 PR 23-AUG-2002; 2002US-0405687P.  
 PR 23-AUG-2002; 2002US-0405698P.  
 PR 26-AUG-2002; 2002US-0406353P.  
 XX (AGEE/) AGEE M L.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (BERG/) BERGHS C.  
 PA (BOLD/) BOLDOG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CATT/) CATTERTON E.  
 PA (DIPI/) DIPIPPO V A.  
 PA (EDIN/) EDINGER S R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (GANG/) GANGOLLI E A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (ROTH/) ROTHBERG B G.  
 PA (GUOX/) GUO X S.  
 PA (HERR/) HERRMANN J L.  
 PA (HALV/) HALVORSEN Y.  
 PA (JIWU/) JI W.  
 PA (KEKU/) KEKUDA R.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (LARO/) LAROCHELLE W J.  
 PA (LEPL/) LEPLEY D M.  
 PA (LILL/) LI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (MILL/) MILLER C E.  
 PA (ORTT/) ORT T.  
 PA (PADI/) PADIGARU M.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (PEYM/) PEYMAN J A.  
 PA (RIEG/) RIEGER D K.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (SHEN/) SHENOY S G.  
 PA (SMIT/) SMITHSON G.  
 PA (SPAD/) SPADERNA S K.  
 PA (SPYT/) SPYTEK K A.  
 PA (STON/) STONE D J.  
 PA (TAUP/) TAUPIER R J.  
 PA (VERN/) VERNET C A M.  
 PA (VOSS/) VOSS E Z.  
 PA (ZHON/) ZHONG M.  
 XX  
 PI Agee ML, Alsbrook JP, Anderson DW, Berghs C, Boldog FL,  
 PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;  
 PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;  
 PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV,  
 PI Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;  
 PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Rieger DK;  
 PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;  
 PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;  
 XX  
 DR WPI; 2004-268786/25.  
 DR N-PSDB; ADO42300.  
 XX  
 PT New human NOVX polypeptides and nucleic acid molecules, useful for  
 PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,  
 PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or  
 PT scleroderma.  
 XX  
 PS Claim 1; SEQ ID NO 150; 610pp; English.

XX The invention relates to human NOVX polypeptides and the polynucleotides  
 CC encoding them. The invention also relates to antibodies specific to the  
 CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are  
 CC useful for manufacturing a medicament for treating a syndrome associated  
 CC with a human disease, such as a pathology associated with the NOVX  
 CC polypeptide. The sequences are useful for diagnosing, treating or  
 CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,  
 CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host  
 CC disease, scleroderma, hypertension, haemophilia, idiopathic  
 CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,  
 CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated  
 CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used  
 CC as hybridisation probes, in chromosome mapping, in tissue typing, in  
 CC preventive medicine or in pharmacogenomics. This sequence represents a  
 CC human NOVX polypeptide of the invention.  
 XX  
 SQ Sequence 734 AA;  
 Query Match 97.1%; Score 2980; DB 8; Length 734;  
 Best Local Similarity 78.2%; Pred. No. 9e-269;  
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
 Qy 1 MWGLLLALAAPAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
 Db 1 MWGLLLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
 Qy 61 EOHVRIIRVIKKKVIKKRKKLTLTTRPTPLVTAGPLVTPPTAGTLDPAEKQETCCPLGL 120  
 Db 61 EOHVRIIRVIKKKVIKKRKKLTLTTRPTPLVTAGPLVTPPTAGTLDPAEKQETCCPLGL 120  
 Qy 121 ESLRVSRSRLSEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGCACAEQDQDPWFQVDAGH 180  
 Db 121 ESLRVSRSRLSEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGCACAEQDQDPWFQVDAGH 180  
 Qy 181 PTRFSGVITQGRNSVMRYDWVTSYKQFSNDSRTWGSNRHSSGMDAVFPANSPETPVL 240  
 Db 181 PTRFSGVITQGRNSVMRYDWVTSYKQFSNDSRTWGSNRHSSGMDAVFPANSPETPVL 240  
 Qy 241 NLLPEQVAFIRLLPOTWLOGGAPCLRAILACPSDNDPLFLAEPASSGSDPLDFQHH 300  
 Db 241 NLLPEQVAFIRLLPOTWLOGGAPCLRAILACPSDNDPLFLAEPASSGSDPLDFQHH 300  
 Qy 301 NYKAMRKLMQVQEQCPNITRIYSIGKSYOGLKLYNMEMSDKPGHEHGLGPEVRYVAGMH 360  
 Db 301 NYKAMRKLMQVQEQCPNITRIYSIGKSYOGLKLYNMEMSDKPGHEHGLGPEVRYVAGMH 360  
 Qy 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLSEMRIHLLPSMNPDCGYEIAHRSSELVG 420  
 Db 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLSEMRIHLLPSMNPDCGYEIAHRSSELVG 420  
 Qy 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVFNHHLPLPTVYTLPNATVAPETR 480  
 Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVFNHHLPLPTVYTLPNATVAPETR 480  
 Qy 481 AVIKWMKRIPFVLSANLHGELVVSYPFD----- 509  
 Db 481 AVIKWMKRIPFVLSANLHGELVVSYPFDWTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540  
 Qy 510 -----MVTASGYHSVTRNCVTPREGPPCNFVLTKTPTKORLRELLAAGAKVPP 560  
 Db 510 -----MVTASGYHSVTRNCVTPREGPPCNFVLTKTPTKORLRELLAAGAKVPP 560  
 Qy 541 LAMQDTSRRPCHSQDFSVGHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600  
 Db 541 LAMQDTSRRPCHSQDFSVGHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600  
 Qy 510 ----- 509  
 Db 601 NELPQEWNNKDALTYLEQVRMGIAGVWRDKDTLGIADAVIAVDGINHDVTAMGGDY 660  
 Qy 510 -----MVTASGYHSVTRNCVTPREGPPCNFVLTKTPTKORLRELLAAGAKVPP 560  
 Db 661 WRLLTPTGDMVTASGYHSVTRNCVTPREGPPCNFVLTKTPTKORLRELLAAGAKVPP 720  
 Qy 561 DLRRRLRLRGQKD 574  
 |||||||||

Db	721	DLRRRLRLRCQKD	734	
	RESULT 11			
	ADO42305			
TD	ADO42305	standard; protein; 734 AA.		
XX	AC	ADO42305;		
XX	AC	ADO42305;		
DT	15-JUL-2004	(first entry)		
XX	XX	Human NOVX polypeptide #77.		
DE	Human, NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;			
KW	Parkinson's disease; graft-versus-host disease; scleroderma;			
KW	hyperextension; haemophilia; idiopathic thrombocytopenic purpura;			
KW	immunodeficiency; AIDS; GvS; lipodemia; obesity; Crohn's disease;			
KW	bronchial asthma; anorexia; cancer-associated cachexia;			
KW	multiple sclerosis; fertility.			
XX	XX			
OS	Homo sapiens.			
XX	XX			
FN	US2004058338-A1.			
XX	XX			
PD	25-MAR-2004.			
XX	XX			
XX	02-DEC-2002; 2002US-00307817.			
XX	03-DEC-2001; 2001US-0336881P.			
PR	05-DEC-2001; 2001US-0336820P.			
PR	07-DEC-2001; 2001US-0338285P.			
PR	07-DEC-2001; 2001US-0338318P.			
PR	10-DEC-2001; 2001US-0338989P.			
PR	10-DEC-2001; 2001US-0339022P.			
PR	11-DEC-2001; 2001US-0339214P.			
PR	11-DEC-2001; 2001US-0339316P.			
PR	11-DEC-2001; 2001US-0339517P.			
PR	11-DEC-2001; 2001US-0339611P.			
PR	12-DEC-2001; 2001US-0340981P.			
PR	12-DEC-2001; 2001US-0341346P.			
PR	14-DEC-2001; 2001US-0340390P.			
PR	14-DEC-2001; 2001US-0340440P.			
PR	14-DEC-2001; 2001US-0340565P.			
PR	14-DEC-2001; 2001US-0340608P.			
PR	14-DEC-2001; 2001US-0341144P.			
PR	17-DEC-2001; 2001US-0341477P.			
PR	17-DEC-2001; 2001US-0341540P.			
PR	18-DEC-2001; 2001US-0341768P.			
PR	20-DEC-2001; 2001US-0342592P.			
PR	31-DEC-2001; 2001US-0344903P.			
PR	01-FEB-2002; 2002US-0353286P.			
PR	01-FEB-2002; 2002US-0353288P.			
PR	26-FEB-2002; 2002US-0359599P.			
PR	26-FEB-2002; 2002US-0359626P.			
PR	26-FEB-2002; 2002US-0359671P.			
PR	27-FEB-2002; 2002US-0359914P.			
PR	27-FEB-2002; 2002US-0359956P.			
PR	28-FEB-2002; 2002US-0360924P.			
PR	28-FEB-2002; 2002US-0360964P.			
PR	28-FEB-2002; 2002US-0361028P.			
PR	28-FEB-2002; 2002US-0361264P.			
PR	05-MAR-2002; 2002US-0361264P.			
PR	05-MAR-2002; 2002US-0361770P.			
PR	05-MAR-2002; 2002US-0362308P.			
PR	13-MAR-2002; 2002US-0364181P.			
PR	13-MAR-2002; 2002US-0364238P.			
PR	15-MAR-2002; 2002US-0364978P.			
PR	15-MAR-2002; 2002US-0365025P.			
PR	17-APR-2002; 2002US-0373288P.			
PR	15-MAY-2002; 2002US-0380981P.			
PR	16-MAY-2002; 2002US-0381004P.			
PR	17-MAY-2002; 2002US-0381495P.			
PR	28-MAY-2002; 2002US-0383534P.			
PR	28-MAY-2002; 2002US-0383744P.			
PR	29-MAY-2002; 2002US-0383829P.			
PR	29-MAY-2002; 2002US-0384024P.			
PR	02-JUL-2002; 2002US-0393332P.			
PR	06-AUG-2002; 2002US-0401315P.			
PR	07-AUG-2002; 2002US-0401788P.			
PR	20-AUG-2002; 2002US-0404676P.			
PR	23-AUG-2002; 2002US-0405400P.			
PR	23-AUG-2002; 2002US-0405684P.			
PR	23-AUG-2002; 2002US-0405687P.			
PR	23-AUG-2002; 2002US-0405698P.			
PR	26-AUG-2002; 2002US-0406353P.			
XX	XX			
XX	(AGRE/) AGEE M L.			
PA	(ALSO/) ALSOBOOK J P.			
PA	(ANDE/) ANDERSON D W.			
PA	(BERG/) BERGHS C.			
PA	(BOLD/) BOLDOG F L.			
PA	(BURG/) BURGESS C E.			
PA	(CATT/) CATTERTON E.			
PA	(DIPI/) DIPIPO V A.			
PA	(EDIN/) EDINGER S R.			
PA	(EISE/) EISEN A.			
PA	(ELLE/) ELLERMAN K.			
PA	(GANG/) GANGOLLI E A.			
PA	(GERL/) GERLACH V.			
PA	(GORM/) GORMAN L.			
PA	(ROTH/) ROTHBERG B G.			
PA	(GUOX/) GUO X S.			
PA	(HERR/) HERRMANN J L.			
PA	(HALV/) HALVORSEN Y.			
PA	(JIWV/) JI W.			
PA	(KEKU/) KEKUDA R.			
PA	(KHRA/) KHRAMTSOV N V.			
PA	(LARO/) LAROCHELLE W J.			
PA	(LEPL/) LEPLEY D M.			
PA	(LILL/) LI L.			
PA	(MACD/) MACDOUGALL J R.			
PA	(MILL/) MILLER C E.			
PA	(ORTT/) ORT T.			
PA	(PADI/) PADIGARU M.			
PA	(PATT/) PATTURAJAN M.			
PA	(PENA/) PENNA C E A.			
PA	(PEYM/) PEYMAN J A.			
PA	(RIEG/) RIEGER D K.			
PA	(ROTH/) ROTHENBERG M E.			
PA	(SHEN/) SHENOY S G.			
PA	(SMIT/) SMITHSON G.			
PA	(SPAD/) SPADERNA S K.			
PA	(SPYT/) SPYTEK K A.			
PA	(STON/) STONE D J.			
PA	(TAUP/) TAUPIER R J.			
PA	(VERN/) VERNET C A M.			
PA	(VOSS/) VOSS E Z.			
PA	(ZHON/) ZHONG M.			
XX	XX			
PI	Agee Ml, Alebrook JP, Anderson DW, Berghs C, Boldog FL;			
PI	Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;			
PI	Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;			
PI	Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;			
PI	Larochelle WJ, Lepley DM, Li L, MacDougall JR, Miller CE,			
PI	Padigar M, Patturajan M, Pen CEA, Spaderna S, Rieger DK,			
PI	Rothenberg ME, Sheno S G, Smithson G, Spaderna SK, Spyttek KA;			
XX	Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M,			
DR	WPI; 2004-268786/25.			
DR	N-PSDB; ADO42304.			
XX	XX			
PT	New human NOVX polypeptides and nucleic acid molecules, useful for			
PT	diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,			
PT	atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or			
PT	scleroderma.			
XX	XX			



PS Claim 1; SEQ ID NO 154; 610pp; English.

CC The invention relates to human NOVX polypeptides and the polynucleotides

CC encoding them. The invention also relates to antibodies specific to the

CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are

CC useful for manufacturing a medicament for treating a syndrome associated

CC with a human disease, such as a pathology associated with the NOVX

CC polypeptide. The sequences are useful for diagnosing, treating or

CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,

CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host

CC disease, scleroderma, hypertension, haemophilia, idiopathic

CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,

CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated

CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used

CC as hybridisation probes, in chromosome mapping, in tissue typing, in

CC preventive medicine or in pharmacogenomics. This sequence represents a

CC human NOVX polypeptide of the invention.

XX Sequence 734 AA;

SQ

Query Match 97.1%; Score 2980; DB 8; Length 734;

Best Local Similarity 78.2%; Pred. No. 9e-269;

Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGILLALAPAPANGPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60

Db 1 MWGILLALAPAPANGPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60

Qy 61 EOHVRIIRIVIKKKVIMKKRKKLTTRPTPLVTAGPLVTPPAGTLDPAEKQETCCPPLGL 120

Db 61 EOHVRIIRIVIKKKVIMKKRKKLTTRPTPLVTAGPLVTPPAGTLDPAEKQETCCPPLGL 120

Qy 121 ESLRVSLSLEASSQSFGLGPHRGRNLNIOGLEDGLYDGCAMCAEQDADPWFQVDAGH 180

Db 121 ESLRVSLSLEASSQSFGLGPHRGRNLNIOGLEDGLYDGCAMCAEQDADPWFQVDAGH 180

Qy 181 PTFSGVITGRNSVRYDWVTSYKQVFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240

Db 181 PTFSGVITGRNSVRYDWVTSYKQVFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240

Qy 241 NLPEPOVAFIRLLPOTWLOGGAPCLRAELTACPSDNDLFLAEPASGSSDPLDQHH 300

Db 241 NLPEPOVAFIRLLPOTWLOGGAPCLRAELTACPSDNDLFLAEPASGSSDPLDQHH 300

Qy 301 NYKAMRKLKQVQECNITRIYSIGKSYOGLKLYNMEMSKDKEGHELGEPVRYVAGMH 360

Db 301 NYKAMRKLKQVQECNITRIYSIGKSYOGLKLYNMEMSKDKEGHELGEPVRYVAGMH 360

Qy 361 GNEALGRELLLLMQFLCHFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420

Db 361 GNEALGRELLLLMQFLCHFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420

Qy 421 WAEGRWNNQSIDLNHNFADNLTPLWEAQDQKVPKPHIVPNHHLPLPTTYTTLPNATVAPETR 480

Db 421 WAEGRWNNQSIDLNHNFADNLTPLWEAQDQKVPKPHIVPNHHLPLPTTYTTLPNATVAPETR 480

Qy 481 AVIKWKKRIIPVLISANLHGGELVVSYPFD----- 509

Db 481 AVIKWKKRIIPVLISANLHGGELVVSYPFD----- 509

Qy 510 ----- 509

Db 510 ----- 509

Qy 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCPFTVTVELSCDKFPHE 600

Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCPFTVTVELSCDKFPHE 600

Qy 510 ----- 509

Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTGLGIADAVIADGINHDVTTAWGGDY 660

Qy 510 -----MVTASAEQYSHVTRNCRVTFEEGPPPCNFVLTKTQKRLRELLAAGAKVPP 560

Db 661 WRLLTPGDYMWVTASAEQYSHVTRNCRVTFEEGPPPCNFVLTKTQKRLRELLAAGAKVPP 720

Qy 561 DLRRRLRLRGQKD 574

Db 721 DLRRRLRLRGQKD 734

RESULT 12

ADO42307

ID ADO42307 standard; protein; 734 AA.

XX ADO42307;

XX 15-JUL-2004 (first entry)

XX Human NOVX polypeptide #78.

XX Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;

XX Parkinson's disease; graft-versus-host disease; scleroderma;

XX hypertension; haemophilia; idiopathic thrombocytopenic purpura;

XX immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease;

XX bronchial asthma; anorexia; cancer-associated cachexia;

XX multiple sclerosis; fertility.

XX Homo sapiens.

XX US2004058338-A1.

XX 25-MAR-2004.

XX 02-DEC-2002; 2002US-00307817.

XX 03-DEC-2001; 2001US-0336881P.

XX 05-DEC-2001; 2001US-0336820P.

XX 07-DEC-2001; 2001US-0338285P.

XX 07-DEC-2001; 2001US-0338318P.

XX 10-DEC-2001; 2001US-0338989P.

XX 10-DEC-2001; 2001US-0339022P.

XX 11-DEC-2001; 2001US-0339314P.

XX 11-DEC-2001; 2001US-0339516P.

XX 11-DEC-2001; 2001US-0339517P.

XX 11-DEC-2001; 2001US-0339611P.

XX 12-DEC-2001; 2001US-0340981P.

XX 12-DEC-2001; 2001US-0341346P.

XX 14-DEC-2001; 2001US-0340390P.

XX 14-DEC-2001; 2001US-0340440P.

XX 14-DEC-2001; 2001US-0340565P.

XX 14-DEC-2001; 2001US-0340608P.

XX 14-DEC-2001; 2001US-0341144P.

XX 17-DEC-2001; 2001US-034177P.

XX 17-DEC-2001; 2001US-0341540P.

XX 18-DEC-2001; 2001US-0341768P.

XX 20-DEC-2001; 2001US-0342592P.

XX 31-DEC-2001; 2001US-0344903P.

XX 01-FEB-2002; 2002US-0353286P.

XX 01-FEB-2002; 2002US-0353288P.

XX 26-FEB-2002; 2002US-0359599P.

XX 26-FEB-2002; 2002US-0359626P.

XX 26-FEB-2002; 2002US-0359671P.

XX 27-FEB-2002; 2002US-0359914P.

XX 27-FEB-2002; 2002US-0359856P.

XX 28-FEB-2002; 2002US-0360324P.

XX 28-FEB-2002; 2002US-0360964P.

XX 28-FEB-2002; 2002US-0361028P.

XX 28-FEB-2002; 2002US-0361256P.

XX 05-MAR-2002; 2002US-0361770P.

XX 05-MAR-2002; 2002US-0362230P.

XX 13-MAR-2002; 2002US-0364181P.

XX 13-MAR-2002; 2002US-0364238P.

XX 15-MAR-2002; 2002US-0364978P.

XX 15-MAR-2002; 2002US-0365025P.

XX 17-APR-2002; 2002US-0373288P.

XX 15-MAY-2002; 2002US-0380981P.

XX 16-MAY-2002; 2002US-0381004P.

XX 17-MAY-2002; 2002US-0381495P.



Qy	561	DLRRRLRLRGQKD	574	Db	181	PTRFSGVITQGRNSVMRYDWVTYSYKQV	SNDRTWGSRNHSSQMDAVFPANSDPPTVL	240
Db	721	DLRRRLRLRGQKD	734	Qy	241	NLLPEPOVARFIRLLPOTWLOGGAPCLRAE	ILACPVSDPNDLFLFLEAPASGSSDPLDFQHH	300
RESULT 13								
Id	AAB36174	standard; protein; 734 AA.		Db	241	NLLPEPOVARFIRLLPOTWLOGGAPCLRAE	ILACPVSDPNDLFLFLEAPASGSSDPLDFQHH	300
Ac	AAB36174;			Qy	301	NYKAMRKLMKQVQEQCPNITRIYSIGKSYO	QGLKLYVMEMSDKPGHEHGEPEVRYVAGMH	360
Xx	21-FEB-2001	(first entry)		Db	361	GNEALGREILLLLLMQFLCHEFLRGNPRVT	RLSEMRTHLLPSMNPDCGYETAYHRGSELVG	420
De	Human APG04 protein.			Qy	421	WAEGRWNNQSIDLNHNFPADLNTPLWEAQD	DGKVPHIVPNHHLPLPTTYTLPNATVAPETR	480
Kw	Human; APG04; protease; cytostatic;	immunomodulatory; cancer;		Db	481	AVIKMMKRIPFVLSANLHGGLVVSYPFD		509
Kw	degenerative disorder; antigen processing;	pro-protein processing.		Qy	510	-----	-----	509
Xx	Homo sapiens.			Db	541	LAMQDTSRRPCHSQDFSVHGNIIINGADW	HTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE	600
Xx	US6140098-A.			Qy	510	-----	-----	509
Xx	31-OCT-2000.			Db	601	NELPQEWENKDALITYLEQVRMGIAGV	RDKDTLGIADAVIADGINHDVTTAWGGDY	660
Xx	30-AUG-1996;	96US-00706216.		Qy	510	-----	-----	509
Xx	30-AUG-1996;	96US-00706216.		Db	561	DLRRRLRLRGQKD	574	
Pa	(SCHE ) SCHERING CORP.			Qy	721	DLRRRLRLRGQKD	734	
Pi	Balasubramanian S, Ford J, Zurawski G, Gorman DM;			RESULT 14				
Xx	WPI; 2001-006328/01.			ADJ63969	ADJ63969	standard; protein; 734 AA.		
Dr	N-PSDB; AAC68661.			Id	ADJ63969			
Xx	New nucleic acids encoding proteinases, useful in forensic assays or in			Xx	AC	ADJ63969;		
Pt	situ assays to detect chromosomal abnormalities, or for enhancing the			Xx	DT	06-MAY-2004	(first entry)	
Pt	expression of proteases, which are useful for treating e.g. abnormal			Xx	DE	Human APG04	protease.	
Xx	proliferation.			Xx	Kw	antibody binding; APG04; FDH02; D1B2;	cytostatic; protease;	
Xx	Claim 1; Col 3-8; 35pp; English.			Xx	Kw	genetic fingerprinting; histological marker; cancer;		
Ps	The present sequence is human APG04 protein. The nucleotide sequence			Xx	Kw	degenerative condition; enzyme.		
Cc	encoding this protein is useful in diagnostic kits, forensic assays or in			Xx	OS	Homo sapiens.		
Cc	an in situ assay to detect chromosomal abnormalities. The protein is			Xx	FH	Key	Location/Qualifiers	
Cc	useful for mediating various aspects of cellular physiology or			FT	Peptide	1..21	/note= "Signal peptide"	
Cc	development, e.g. for the conversion of pro-proteins to proteins, or for			FT	Protein	22..734	/note= "Mature protein"	
Cc	proper immunological function, antigen processing and presentation. The			FT	Active-site	360	/note= "Zinc chelating residue"	
Cc	protein or its fragments is useful in treating conditions associated with			FT	Active-site	363	/note= "Zinc chelating residue"	
Cc	abnormal physiology or development, e.g. abnormal proliferation in			FT	Active-site	385	/note= "Zinc chelating residue"	
Cc	cancerous conditions, or degenerative conditions. The nucleic acids and			FT	Active-site	398	/note= "Zinc chelating residue"	
Cc	proteins are also useful for drug screening techniques			FT				
Xx	Sequence 734 AA;			XX				
SQ	Query Match	96.9%; Score 2976; DB 4; Length 734;		XX				
	Best Local Similarity	78.1%; Pred. No. 2.1e-268;		XX				
	Matches 573; Conservative	1; Mismatches 0; Indels 160; Gaps 1;		XX				
Qy	1	MWGLLLAALAPAVGALCAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS	60	FT				
Db	1	MWGLLLAALAPAVGALCAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS	60	FT				
Qy	61	EQHVRIRVIKKKVIKKRKLTLTRETPLVTAGPLVTPPTAGTLDPAEQKQETGCPPLGL	120	FT				
Db	61	EQHVRIRVIKKKVIKKRKLTLTRETPLVTAGPLVTPPTAGTLDPAEQKQETGCPPLGL	120	FT				
Qy	121	ESLRVDSRLAESSSQFGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH	180	FT				
Db	121	ESLRVDSRLAESSSQFGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH	180	FT				
Qy	181	PTRFSGVITQGRNSVMRYDWVTYSYKQV	SNDRTWGSRNHSSQMDAVFPANSDPPTVL	240	FT			

PF 29-AUG-2000; 2000US-00650284.  
XX 30-AUG-1996; 96US-00706216.  
XX (SCHE) SCHERING CORP.  
XX Balasubramanian S, Ford J, Gorman DM, Zurawski G;  
XX WPI, 2003-842784/78.  
XX N-FSDB; ADJ63968.  
XX New compounds comprising antibody binding site specific for human APG04  
XX FDH02 or DIB2 protein, useful for treating conditions associated with  
XX abnormal physiology or development, e.g. cancerous or degenerative  
XX conditions.  
XX Disclosure; Col 53-56; 35pp; English.  
XX This invention relates to a novel binding compound comprising an antibody ly  
XX binding site which specifically a human APG04, FDH02 or DIB2 protein. The  
XX compound of the invention may have cytotstatic and protease activities.  
XX The binding compounds of the invention may be used in standard procedures  
XX to isolate genes from different individuals or other species, in forens c  
XX assays (e.g. in genetic fingerprinting), as histological markers, or in  
XX treating conditions associated with abnormal physiology or development,  
XX including abnormal proliferation, e.g. cancerous or degenerative  
XX conditions. The present sequence represents the human APG04 protease  
XX which binds to the antibody binding compound of the invention.  
XX Sequence 734 AA;  
SQ  
Query Match 96.9%; Score 2976; DB 7; Length 734;  
Best Local Similarity 78.1%; Pred. No. 2.le-268;  
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;  
QY 1 MWGLLALAAFAVAPALCAPNSVLGLAQPTTKVPGSTPALHSSPAQPAETANGTS 6  
DB 1 MWGLLALAAFAVAPALCAPNSVLGLAQPTTKVPGSTPALHSSPAQPAETANGTS 6  
QY 61 EQHVRIRVIKKKVIKKRKKLTTRPTPLTAGPLVTTTPTAGTLPBAEKQSTGCPPLGL 1 0  
DB 61 EQHVRIRVIKKKVIKKRKKLTTRPTPLTAGPLVTTTPTAGTLPBAEKQSTGCPPLGL 1 0  
QY 121 ESLRVSLSRLAASSQSFGLPGRHRLNIQSGLEDGLYDGAWCAEEQADDPFQVDAGH 1 0  
DB 121 ESLRVSLSRLAASSQSFGLPGRHRLNIQSGLEDGLYDGAWCAEEQADDPFQVDAGH 1 0  
QY 181 PTFSGVITQGRNSVWRVYDWTYSYKQFNSDRTWGSNSHSGMDVFPANSDPETVL 2 0  
DB 181 PTFSGVITQGRNSVWRVYDWTYSYKQFNSDRTWGSNSHSGMDVFPANSDPETVL 2 0  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDNDLFLAPASGSDPLDFQHH 3 0  
DB 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDNDLFLAPASGSDPLDFQHH 3 0  
QY 301 NYKAMEKLMKQVEQCPNTRIYSYKSGYOGI KLYMMSDKPGHEHGEPEVRYVAGMH 3 0  
DB 301 NYKAMEKLMKQVEQCPNTRIYSYKSGYOGI KLYMMSDKPGHEHGEPEVRYVAGMH 3 0  
QY 361 GNEALGRELLLMQFLCHEFIRGPRVTRLLSEMRHLLPSMNDPDGYEIAHYRGSSELV 4 0  
DB 361 GNEALGRELLLMQFLCHEFIRGPRVTRLLSEMRHLLPSMNDPDGYEIAHYRGSSELV 4 0  
QY 421 WAEGRWNSQIDINHNADLNTPLNEAODGKPHIVNHHLLPLPTYYTLNATVAPETR 4 0  
DB 421 WAEGRWNSQIDINHNADLNTPLNEAODGKPHIVNHHLLPLPTYYTLNATVAPETR 4 0  
QY 481 AVIKMKKIRPVL SANHGGELVWSYDPTD----- 50  
DB 481 AVIKMKKIRPVL SANHGGELVWSYDPTDPTPWAARELTPTDPAVRLWLTSTVYAGSN 54  
QY 510 ----- 50

Db 541 LAMQDTSRRPCHSQDFSVHGNIIINGADWHITVPGSMNDSYLTHTNCFEVTVELSCDKFPHE 600  
QY 510 ----- 509  
Db 601 NELPQEWENNKDALLTYLEQVPMGTAGVVRDKDTGLGTADAVIADVGINHDVTTAWGGDY 660  
QY 510 -----MVTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORIRELLAAGAKVPP 560  
Db 661 WRLLTPGDYMTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORIRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGOKD 574  
Db 721 DLRRRLRLRGOKD 734  
RESULT 15  
AAU29252  
ID AAU29252 standard, protein; 734 AA.  
XX AAU29252;  
AC AAU29252;  
DT 18-DEC-2001 (first entry)  
XX Human PRO polypeptide sequence #229.  
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX Homo sapiens.  
XX WO20016848-A2.  
XX 20-SEP-2001.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 03-MAR-2000; 2000US-0187202P.  
XX 06-MAR-2000; 2000US-0186968P.  
XX 14-MAR-2000; 2000US-0189320P.  
XX 15-MAR-2000; 2000US-0189328P.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 21-MAR-2000; 2000US-0191007P.  
XX 21-MAR-2000; 2000US-0191048P.  
XX 21-MAR-2000; 2000US-0191314P.  
XX 28-MAR-2000; 2000US-0192655P.  
XX 29-MAR-2000; 2000US-0193032P.  
XX 30-MAR-2000; 2000US-0193053P.  
XX 04-APR-2000; 2000WO-US008439.  
XX 04-APR-2000; 2000US-0194449P.  
XX 11-APR-2000; 2000US-0194647P.  
XX 11-APR-2000; 2000US-0195975P.  
XX 11-APR-2000; 2000US-0196000P.  
XX 11-APR-2000; 2000US-0196187P.  
XX 11-APR-2000; 2000US-0196690P.  
XX 18-APR-2000; 2000US-0196820P.  
XX 18-APR-2000; 2000US-0198121P.  
XX 25-APR-2000; 2000US-0199397P.  
XX 25-APR-2000; 2000US-0199550P.  
XX 03-MAY-2000; 2000US-0201516P.  
XX 17-MAY-2000; 2000WO-US013705.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2001-602746/68.  
DR N-FSD8; AAS46153.  
DR  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.  
XX  
PS Claim 11; Fig 458; 774pp; English.  
XX  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX  
SQ Sequence 734 AA;  
Query Match 96.9%; Score 2975; DB 4; Length 734;  
Best Local Similarity 78.1%; Pred. No. 2.6e-268;  
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;  
QY 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
Db 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EOHVRIKVIKKKVIKMKRKKLTLTRETPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120  
Db 61 EOHVRIKVIKKKVIKMKRKKLTLTRETPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120  
QY 121 ESLRVSDSRLEASSQSFGLGPHRGRLNIOSGLEGDGLYDGAWCAEQDADPWFQVDAGH 180  
Db 121 ESLRVSDSRLEASSQSFGLGPHRGRLNIOSGLEGDGLYDGAWCAEQDADPWFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFNSDRTWGSNRHSSGMDAVFPANSDPETPVL 240  
Db 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFNSDRTWGSNRHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPDNDLFLFAPASGSSDPLDFQHH 300  
Db 241 NLLPEQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPDNDLFLFAPASGSSDPLDFQHH 300  
QY 301 NYKAMRKLKQVQCCPNITRIYSIGKSYOGLKLYNMEMSDKPGCHELGRPEVRYVAGMH 360  
Db 301 NYKAMRKLKQVQCCPNITRIYSIGKSYOGLKLYNMEMSDKPGCHELGRPEVRYVAGMH 360  
QY 361 GNEALGRELILLMLQFLCHEFLGRGNPRVTRILLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
Db 361 GNEALGRELILLMLQFLCHEFLGRGNPRVTRILLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
QY 421 WAGRWNNQSIDLNHNFADLNTPLWEAQDQKGVPHIVPNHHLPLPTTYTLPNATVAPETR 480  
Db 421 WAGRWNNQSIDLNHNFADLNTPLWEAQDQKGVPHIVPNHHLPLPTTYTLPNATVAPETR 480

QY 481 AVIKWMKRIIPFVLSANLHGGELVVSYPFD----- 509  
Db 481 AVIKWMKRIIPFVLSANLHGGELVVSYPFDTRTPWAARELTTPDDAVFRWLSTVYAGSN 540  
QY 510 ----- 509  
Db 541 LAMQDTSRRPCHSQDFSVHGNIIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600  
QY 510 ----- 509  
Db 601 NELPQEWENKDALLLTYLEQVRMGIAGVVRDKOTELGIADAVIAVDGINHDVTTAMGGDY 660  
QY 510 -----MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 560  
Db 661 WRLLTPGDYMTASAEGYHSVTENCRCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db 721 DLRRRLRLRGQKD 734

Search completed: January 10, 2005, 19:33:57  
Job time : 162 secs

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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:37:37 ; Search time 147 Seconds  
(without alignments)

1407.945 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLLAALAFAPAVGALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pdb.\*

2: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pdb.\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW PUB.pdb.\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pdb.\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW PUB.pdb.\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pdb.\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW PUB.pdb.\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pdb.\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pdb.\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pdb.\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pdb.\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW PUB.pdb.\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pdb.\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pdb.\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pdb.\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pdb.\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW PUB.pdb.\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW PUB.pdb.\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW PUB.pdb.\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3070	100.0	574	10	US-09-996-015-6
2	3070	100.0	574	15	US-10-287-190-170
3	3070	100.0	574	15	US-10-307-817-152
4	2980	97.1	734	10	US-09-996-015-2
5	2980	97.1	734	14	US-10-239-663-65
6	2980	97.1	734	15	US-10-287-190-168
7	2980	97.1	734	15	US-10-287-190-174
8	2980	97.1	734	15	US-10-307-817-150
9	2980	97.1	734	15	US-10-307-817-154
10	2980	97.1	734	15	US-10-307-817-156
11	2976	96.9	734	10	US-09-813-432-38
12	2976	96.9	734	14	US-10-174-364-38
13	2976	96.9	734	15	US-10-246-583-38

14	2976	96.9	734	16	US-10-689-832-38	Sequence 38, Appl
15	2975	96.9	734	13	US-10-052-586-458	Sequence 58, App
16	2975	96.9	734	14	US-10-174-590-458	Sequence 458, App
17	2975	96.9	734	14	US-10-176-758-458	Sequence 458, App
18	2975	96.9	734	14	US-10-175-737-458	Sequence 458, App
19	2975	96.9	734	14	US-10-174-581-458	Sequence 458, App
20	2975	96.9	734	14	US-10-176-483-458	Sequence 458, App
21	2975	96.9	734	14	US-10-176-749-458	Sequence 458, App
22	2975	96.9	734	14	US-10-176-914-458	Sequence 458, App
23	2975	96.9	734	14	US-10-173-706-458	Sequence 458, App
24	2975	96.9	734	14	US-10-175-738-458	Sequence 458, App
25	2975	96.9	734	14	US-10-175-752-458	Sequence 458, App
26	2975	96.9	734	14	US-10-176-482-458	Sequence 458, App
27	2975	96.9	734	14	US-10-176-757-458	Sequence 458, App
28	2975	96.9	734	14	US-10-176-913-458	Sequence 458, App
29	2975	96.9	734	14	US-10-180-552-458	Sequence 458, App
30	2975	96.9	734	14	US-10-173-706-458	Sequence 458, App
31	2975	96.9	734	14	US-10-175-738-458	Sequence 458, App
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33	2975	96.9	734	14	US-10-176-482-458	Sequence 458, App
34	2975	96.9	734	14	US-10-176-749-458	Sequence 458, App
35	2975	96.9	734	14	US-10-176-914-458	Sequence 458, App
36	2975	96.9	734	14	US-10-173-706-458	Sequence 458, App
37	2975	96.9	734	14	US-10-175-738-458	Sequence 458, App
38	2975	96.9	734	14	US-10-175-752-458	Sequence 458, App
39	2975	96.9	734	14	US-10-176-482-458	Sequence 458, App
40	2975	96.9	734	14	US-10-176-749-458	Sequence 458, App
41	2975	96.9	734	14	US-10-176-914-458	Sequence 458, App
42	2975	96.9	734	14	US-10-173-706-458	Sequence 458, App
43	2975	96.9	734	14	US-10-175-738-458	Sequence 458, App
44	2975	96.9	734	14	US-10-175-752-458	Sequence 458, App
45	2975	96.9	734	14	US-10-176-482-458	Sequence 458, App

ALIGNMENTS

RESULT 1

US-09-996-015-6

; Sequence 6, Application US/09996015

; Publication No. US20030032166A1

; GENERAL INFORMATION:

; APPLICANT: Quinn, Kerry E.

; APPLICANT: Pena, Carol A. E.

; APPLICANT: Li, Li

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Leite, Marlo W.

; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids

; FILE REFERENCE: 15966-581 CIP

; CURRENT APPLICATION NUMBER: US/09/996,015

; CURRENT FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: 09/641,741

; PRIOR FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: 60/159,613

; PRIOR FILING DATE: 1999-10-14

; PRIOR APPLICATION NUMBER: 60/175,534

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 60/224,086

; PRIOR FILING DATE: 2000-08-09

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 574

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-015-6

Query Match 100.0%; Score 3070; DB 10; Length 574;  
Best Local Similarity 100.0%; Pred. No. 2e-259;  
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLLLAALAFAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPAETANGTS 60

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Db      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 1
Qy      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 1:0
Db      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 1:0
Qy      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 1:0
Db      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 1:0
Qy      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 2 0
Db      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 2 0
Qy      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 3 0
Db      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 3 0
Qy      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 3 0
Db      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 3 0
Qy      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 4 0
Db      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 4 0
Qy      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 4:0
Db      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 4:0
Qy      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 5 0
Db      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 5 0
Qy      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
Db      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

RESULT 2
US-10-287-190-170
; Sequence 170, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-780B
; CURRENT APPLICATION NUMBER: US/10/287,190
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 09/996,015
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/338626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/373806
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/338196
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/333912
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/381043
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/401593
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/334300
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 170
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-190-170

Db      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 1
Qy      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 1:0
Db      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 1:0
Qy      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 1:0
Db      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 1:0
Qy      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 2 0
Db      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 2 0
Qy      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 3 0
Db      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 3 0
Qy      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 3 0
Db      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 3 0
Qy      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 4 0
Db      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 4 0
Qy      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 4:0
Db      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 4:0
Qy      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 5 0
Db      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 5 0
Qy      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
Db      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

RESULT 3
US-10-307-817-152
; Sequence 152, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 152
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-152

Query Match      100.0%; Score 3070; DB 15; Length 574;
Best Local Similarity      100.0%; Pred. No. 2e-259;
Matches 574; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
Db      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
Qy      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 180
Db      121 ESLRVSDSLRLSASSQSFGLGPHRGRNLNIOGLEDGDLYGAWCAEEOQADPWFOVDAGH 180
Qy      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 240
Db      181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWMSRNHSSGMDAVFPANSDPETPVL 240
Qy      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 300
Db      241 NLLPEPOVARFIRLLPOTWLOGGAPCLRAETILACVSDPNDFLEAPASGSSDPLDFQHH 300
Qy      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db      301 NYKAMRKLKMKQVQCCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Qy      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 420
Db      361 GNEALGRELLLLMQFLCHEFELRGNPRVTRLLSEMRTHLLPSMNPDPGYEIAHHRGSELV 420
Qy      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 480
Db      421 WAEGRWNNQSIDLNHNFDADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYYTLFNATVAPETR 480
Qy      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 540
Db      481 AVIKMKRIRIPFVLSANLHGSELVVSYPDMVTASAEGYHSVTRNCRVTFEEGPPFCNFVL 540
Qy      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
Db      541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

Query Match      100.0%; Score 3070; DB 15; Length 574;
Best Local Similarity      100.0%; Pred. No. 2e-259;
Matches 574; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db      1 MWGLLLAALAAFAFAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy      61 EQHVRIRIVIKKKVKIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
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Db 61 EQHVRIRVIKKKKVIMKKRKKLLTLTRPTPLVATAGPLVTPAGTLDPAEKQETGCPPLGL 120  
QY 121 ESLRVSRSLEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180  
Db 121 ESLRVSRSLEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180  
QY 181 PTFSGVITQGRNSVMRYDWMVTSYKQVFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240  
Db 181 PTFSGVITQGRNSVMRYDWMVTSYKQVFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300  
Db 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300  
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGSKYQGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
Db 301 NYKAMRKLKMQVOEQCPNITRIYSIGSKYQGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAHRGSELVG 420  
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAHRGSELVG 420  
QY 421 WABGRWNQSIDLNHNFADLNTPLWEAQDDGKVPPIVPHNHHLLPLPTYYTLPNATVAPETR 480  
Db 421 WABGRWNQSIDLNHNFADLNTPLWEAQDDGKVPPIVPHNHHLLPLPTYYTLPNATVAPETR 480  
QY 481 AVTKMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHVSVTRNCRVTPEEGPPPCNFVL 540  
Db 481 AVTKMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHVSVTRNCRVTPEEGPPPCNFVL 540  
QY 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574  
Db 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

RESULT 4

US-09-996-015-2  
; Sequence 2, Application US/09996015  
; Publication No. US20030032166A1  
; GENERAL INFORMATION:  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Pena, Carol A. E.  
; APPLICANT: Li, Li  
; APPLICANT: Spaderna, Steven K.  
; APPLICANT: Leite, Marlo W.  
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids  
; FILE REFERENCE: Encoding Same  
; FILE REFERENCE: 15966-581 CIP  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 09/641,741  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/159,613  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 60/175,534  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/224,086  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-015-2  
Query Match 97.1%; Score 2980; DB 10; Length 734;  
Best Local Similarity 78.2%; Pred. No. 2.2e-251;  
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
QY 1 MWGLLLAALAFAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Db 1 MWGLLLAALAFAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EQHVRIRVIKKKKVIMKKRKKLLTLTRPTPLVATAGPLVTPAGTLDPAEKQETGCPPLGL 120  
Db 61 EQHVRIRVIKKKKVIMKKRKKLLTLTRPTPLVATAGPLVTPAGTLDPAEKQETGCPPLGL 120  
QY 121 ESLRVSRSLEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180  
Db 121 ESLRVSRSLEASSSQSFGGLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180  
QY 181 PTFSGVITQGRNSVMRYDWMVTSYKQVFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240  
Db 181 PTFSGVITQGRNSVMRYDWMVTSYKQVFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300  
Db 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300  
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGSKYQGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
Db 301 NYKAMRKLKMQVOEQCPNITRIYSIGSKYQGLKLYNMESDKPGEHELGEPEVRYVAGMH 360  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAHRGSELVG 420  
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAHRGSELVG 420  
QY 421 WABGRWNQSIDLNHNFADLNTPLWEAQDDGKVPPIVPHNHHLLPLPTYYTLPNATVAPETR 480  
Db 421 WABGRWNQSIDLNHNFADLNTPLWEAQDDGKVPPIVPHNHHLLPLPTYYTLPNATVAPETR 480  
QY 481 AVTKMKRIPFVLSANLHGGLVVSYPFD----- 509  
Db 481 AVTKMKRIPFVLSANLHGGLVVSYPFDWTRTPWAARELTPTDDAVFRWLSTVYAGSN 540  
QY 510 ----- 509  
Db 541 LAMQDTSRRRCHSQDFSVMGNIINGADWHTVPGSMNDFSYLHNTNCFVTVELSCDKPPHE 600  
QY 510 ----- 509  
Db 601 NELPQEWENNKDALLTYLQVRMGIAGVVRDKDELGIADAVDGINHDVTTAWGDDY 660  
QY 510 -----MVTASAGYHVSVTRNCRVTPEEGPPPCNFVLTKTPKQRLRELLAAGAKVPP 560  
Db 661 WRLLTPGDYMTASAGYHVSVTRNCRVTPEEGPPPCNFVLTKTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db 721 DLRRRLRLRGQKD 734

RESULT 5

US-10-239-663-65  
; Sequence 65, Application US/10239663  
; Publication No. US20030139572A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia, K.  
; APPLICANT: Smith, Randall, F.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Kabnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/10/239,663  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166

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; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-663-65

Query Match      97.1%; Score 2980; DB 14; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 61
Db 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 61
QY 61 EHVRIIRIVIKKKVIMKKRKKLTTRTPPLVTAGPLVTPTPAETLPAEKQETGCPPLGL 10
Db 61 EHVRIIRIVIKKKVIMKKRKKLTTRTPPLVTAGPLVTPTPAETLPAEKQETGCPPLGL 10
QY 121 ESLRVSRLSEASSQSFGLPGRHRLNIQSGLEDGLYDGCAMCAEQDADPWFQVDAGH 10
Db 121 ESLRVSRLSEASSQSFGLPGRHRLNIQSGLEDGLYDGCAMCAEQDADPWFQVDAGH 10
QY 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWGSRNHSSGMDAVFPANSDPETVL 20
Db 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWGSRNHSSGMDAVFPANSDPETVL 20
QY 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 30
Db 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 30
QY 301 NYKAMRKLKMQVQSCPNITRIYSIGSKYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 30
Db 301 NYKAMRKLKMQVQSCPNITRIYSIGSKYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 30
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEIAHRSGLVG 40
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEIAHRSGLVG 40
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHPHVPNNHLLPLPTYYTLPNATVAPETR 40
Db 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHPHVPNNHLLPLPTYYTLPNATVAPETR 40
QY 481 AVIKWKKRIIPFVLSANLHGELVVSYPFD-----509
Db 481 AVIKWKKRIIPFVLSANLHGELVVSYPFD-----509
QY 510 -----509
Db 541 LAMQDTSRRPCHSQDFSFGHNGIINGADWHTVPGSMNDFSYLHTNCFEVTVLSKDPFHE 600
QY 510 -----509

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; FILE REFERENCE: 21402-780B
; CURRENT APPLICATION NUMBER: US/10/287,190
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 09/996,015
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/338626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/373806
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/338196
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/333912
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/381043
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/401593
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/334300
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 168
; TYPE: PRT
; LENGTH: 734
; ORGANISM: Homo sapiens
US-10-287-190-168

Query Match      97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EHVRIIRIVIKKKVIMKKRKKLTTRTPPLVTAGPLVTPTPAETLPAEKQETGCPPLGL 120
Db 61 EHVRIIRIVIKKKVIMKKRKKLTTRTPPLVTAGPLVTPTPAETLPAEKQETGCPPLGL 120
QY 121 ESLRVSRLSEASSQSFGLPGRHRLNIQSGLEDGLYDGCAMCAEQDADPWFQVDAGH 180
Db 121 ESLRVSRLSEASSQSFGLPGRHRLNIQSGLEDGLYDGCAMCAEQDADPWFQVDAGH 180
QY 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWGSRNHSSGMDAVFPANSDPETVL 240
Db 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWGSRNHSSGMDAVFPANSDPETVL 240
QY 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 300
Db 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 300
QY 301 NYKAMRKLKMQVQSCPNITRIYSIGSKYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVQSCPNITRIYSIGSKYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEIAHRSGLVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEIAHRSGLVG 420
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHPHVPNNHLLPLPTYYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHPHVPNNHLLPLPTYYTLPNATVAPETR 480
QY 481 AVIKWKKRIIPFVLSANLHGELVVSYPFD-----509
Db 481 AVIKWKKRIIPFVLSANLHGELVVSYPFD-----509
QY 510 -----509
Db 541 LAMQDTSRRPCHSQDFSFGHNGIINGADWHTVPGSMNDFSYLHTNCFEVTVLSKDPFHE 600
QY 510 -----509

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RESULT 6
US-10-287-190-168
; Sequence 168, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

```

Db 601 NELPQEWNNKDALTYLQVNRMGIAGVVRDKDTLGIADAVIADVGINHDTVTTAMGGDY 660  
QY 510 -----MVTASAEYHSVTRNCRVTFEEGPPFCNFKVLTTPKQRLRELLAAGAKVPP 560  
Db 661 WRLLTQGDYMWVTASAEYHSVTRNCRVTFEEGPPFCNFKVLTTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db 721 DLRRRLRLRGQKD 734  
RESULT 7  
US-10-287-190-174  
; Sequence 174, Application US/10287190  
; Publication No. US20040038230A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John P. et al.  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-780B  
; CURRENT APPLICATION NUMBER: US/10/287,190  
; CURRENT FILING DATE: 2003-04-02  
; PRIOR APPLICATION NUMBER: 09/996,015  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/338626  
; PRIOR FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: 60/373806  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/338196  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/333912  
; PRIOR FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/381043  
; PRIOR FILING DATE: 2002-05-16  
; PRIOR APPLICATION NUMBER: 60/401593  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: 60/334300  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 174  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-190-174  
Query Match 97.1%; Score 2980; DB 15; Length 734;  
Best Local Similarity 78.2%; Pred. No. 2.2e-251;  
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
QY 1 MWGLLLAALAAFAVAVGPAVGALGAPRNSVLGLAQPGTTTKVPGSTPALHSSPAQPPAETANGTS 60  
Db 1 MWGLLLAALAAFAVAVGPAVGALGAPRNSVLGLAQPGTTTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EQHVRIRVTKKKVIMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPAAKQETGCPPLGL 120  
Db 61 EQHVRIRVTKKKVIMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPAAKQETGCPPLGL 120  
QY 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNQSGLDGLYDGAWCABEQDADPMFQVDAGH 180  
Db 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNQSGLDGLYDGAWCABEQDADPMFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240  
Db 181 PTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300  
Db 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300  
QY 301 NYKAMKLMKQVQEQCPNITRIYSICKSYOGLKLYNEMSDKPGHELGEPEVRYVAGMH 360  
Db 301 NYKAMKLMKQVQEQCPNITRIYSICKSYOGLKLYNEMSDKPGHELGEPEVRYVAGMH 360

QY 361 GNEALGRELLELLLMQFLCHEFLRGNPRVTRLSEMRIHLPSMNPDCGYEYAIHRGSELVG 420  
Db 361 GNEALGRELLELLLMQFLCHEFLRGNPRVTRLSEMRIHLPSMNPDCGYEYAIHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNRNFADLNTPLWEAODDGKVPHVNPVNHLLPLPTTYTILPNATVAETR 480  
Db 421 WAEGRWNNQSIDLNRNFADLNTPLWEAODDGKVPHVNPVNHLLPLPTTYTILPNATVAETR 480  
QY 481 AVIKMMKRIPPFVLSANLHGGLVVSYPFD----- 509  
Db 481 AVIKMMKRIPPFVLSANLHGGLVVSYPFDWTRTPWAARELTPTPDADDVFRWLSTVYAGSN 540  
QY 510 ----- 509  
Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCEVTVELSCDKPPHE 600  
QY 510 ----- 509  
Db 601 NELPQEWNNKDALTYLQVNRMGIAGVVRDKDTLGIADAVIADVGINHDTVTTAMGGDY 660  
QY 510 -----MVTASAEYHSVTRNCRVTFEEGPPFCNFKVLTTPKQRLRELLAAGAKVPP 560  
Db 661 WRLLTQGDYMWVTASAEYHSVTRNCRVTFEEGPPFCNFKVLTTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db 721 DLRRRLRLRGQKD 734  
RESULT 8  
US-10-307-817-150  
; Sequence 150, Application US/10307817  
; Publication No. US20040058338A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-502C  
; CURRENT APPLICATION NUMBER: US/10/307,817  
; CURRENT FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 682  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 150  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-307-817-150  
Query Match 97.1%; Score 2980; DB 15; Length 734;  
Best Local Similarity 78.2%; Pred. No. 2.2e-251;  
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;  
QY 1 MWGLLLAALAAFAVAVGPAVGALGAPRNSVLGLAQPGTTTKVPGSTPALHSSPAQPPAETANGTS 60  
Db 1 MWGLLLAALAAFAVAVGPAVGALGAPRNSVLGLAQPGTTTKVPGSTPALHSSPAQPPAETANGTS 60  
QY 61 EQHVRIRVTKKKVIMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPAAKQETGCPPLGL 120  
Db 61 EQHVRIRVTKKKVIMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPAAKQETGCPPLGL 120  
QY 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNQSGLDGLYDGAWCABEQDADPMFQVDAGH 180  
Db 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNQSGLDGLYDGAWCABEQDADPMFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240  
Db 181 PTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300  
Db 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300  
QY 301 NYKAMKLMKQVQEQCPNITRIYSICKSYOGLKLYNEMSDKPGHELGEPEVRYVAGMH 360  
Db 301 NYKAMKLMKQVQEQCPNITRIYSICKSYOGLKLYNEMSDKPGHELGEPEVRYVAGMH 360

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Db 301 NYKAMRKLKMQVQOCNPNIIRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 3 0
Qy 361 GNEALGRELLLLLMQFLCHEFIRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSELVG 4 0
Db 361 GNEALGRELLLLLMQFLCHEFIRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSELVG 4 0
Qy 421 WAEGRWNNQSIDLNNHFNADLNTPLMEAQDQGVPHIHPNNHLLPLPTYYTLPNATVAPETR 4 0
Db 421 WAEGRWNNQSIDLNNHFNADLNTPLMEAQDQGVPHIHPNNHLLPLPTYYTLPNATVAPETR 4 0
Qy 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 5 9
Db 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTPTPWAARELTPTDDAVERWLSVTVAGSN 5 0
Qy 510 ----- 5 9
Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHNTCFEVTVELSCDKFPHE 6 0
Qy 510 ----- 5 9
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGLIADAVIADVGINHDVTTAWGGDY 6 0
Qy 510 -----MVTASAEGYHSVTRNCRVTPPEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 5 0
Db 661 WRLLTPGDYMYVTASAEGYHSVTRNCRVTPPEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 7 0
Qy 561 DLRRRLERLRGOKD 574
Db 721 DLRRRLERLRGOKD 734

RESULT 9
US-10-307-817-154
; Sequence 154, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 154
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-154

Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAAPAVGPAVGPAAGPAPNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 6'
Db 1 MWGLLLAALAAPAVGPAVGPAAGPAPNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 6'
Qy 61 EOHVRIIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 1' 0
Db 61 EOHVRIIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 1' 0
Qy 121 ESLRVSLSRLEASSQSFGLGPHRGLNIOGLEDGLDYDGAKCAEODADPWFQVDAGH 1' 0
Db 121 ESLRVSLSRLEASSQSFGLGPHRGLNIOGLEDGLDYDGAKCAEODADPWFQVDAGH 1' 0
Qy 181 PTRFSGVITQGRNSVWRVYDWTYSYKQFSDNRSRTWWSRNHSSGMDAVFPANSPETPVL 2' 0
Db 181 PTRFSGVITQGRNSVWRVYDWTYSYKQFSDNRSRTWWSRNHSSGMDAVFPANSPETPVL 2' 0
Qy 241 NLLPPEQVARFIRLLPQTLWLOGGACPLRAETILACVPSPNDLFLFAPASGSDPLDFQHH 3' 0
Db 241 NLLPPEQVARFIRLLPQTLWLOGGACPLRAETILACVPSPNDLFLFAPASGSDPLDFQHH 3' 0
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```
Qy 301 NYKAMRKLKMQVQOCNPNIIRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVQOCNPNIIRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Qy 361 GNEALGRELLLLLMQFLCHEFIRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSELVG 420
Db 361 GNEALGRELLLLLMQFLCHEFIRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSELVG 420
Qy 421 WAEGRWNNQSIDLNNHFNADLNTPLMEAQDQGVPHIHPNNHLLPLPTYYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNNHFNADLNTPLMEAQDQGVPHIHPNNHLLPLPTYYTLPNATVAPETR 480
Qy 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 509
Db 481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTPTPWAARELTPTDDAVERWLSVTVAGSN 540
Qy 510 ----- 509
Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHNTCFEVTVELSCDKFPHE 600
Qy 510 ----- 509
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGLIADAVIADVGINHDVTTAWGGDY 660
Qy 510 -----MVTASAEGYHSVTRNCRVTPPEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 560
Db 661 WRLLTPGDYMYVTASAEGYHSVTRNCRVTPPEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLERLRGOKD 574
Db 721 DLRRRLERLRGOKD 734

RESULT 10
US-10-307-817-156
; Sequence 156, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 156
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-156

Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAAPAVGPAVGPAAGPAPNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAAPAVGPAVGPAAGPAPNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EOHVRIIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
Db 61 EOHVRIIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
Qy 121 ESLRVSLSRLEASSQSFGLGPHRGLNIOGLEDGLDYDGAKCAEODADPWFQVDAGH 180
Db 121 ESLRVSLSRLEASSQSFGLGPHRGLNIOGLEDGLDYDGAKCAEODADPWFQVDAGH 180
Qy 181 PTRFSGVITQGRNSVWRVYDWTYSYKQFSDNRSRTWWSRNHSSGMDAVFPANSPETPVL 240
Db 181 PTRFSGVITQGRNSVWRVYDWTYSYKQFSDNRSRTWWSRNHSSGMDAVFPANSPETPVL 240
Qy 241 NLLPPEQVARFIRLLPQTLWLOGGACPLRAETILACVPSPNDLFLFAPASGSDPLDFQHH 300
Db 241 NLLPPEQVARFIRLLPQTLWLOGGACPLRAETILACVPSPNDLFLFAPASGSDPLDFQHH 300
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Db 241 NLLPEQVAPRIRLLPQTWLGQAPCLRAEILACPVSDDPNDLFLLEAPASGSSDPLDFQHH 300  
Qy 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGCEHELGEPEVRYVAGMH 360  
Db 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGCEHELGEPEVRYVAGMH 360  
Qy 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
Db 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
Qy 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPYHIVPNHHLPLPTYTYTLPNATVAPETR 480  
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPYHIVPNHHLPLPTYTYTLPNATVAPETR 480  
Qy 481 AVIKMKRKIPFVLSANLHGELVVSYPFD----- 509  
Db 481 AVIKMKRKIPFVLSANLHGELVVSYPFD----- 540  
Qy 510 ----- 509  
Db 541 LAMQDTSRRPCHSQDPSVHGNIINGADWHTVPGSMNDFSYLHTNCPVTVVELSCDKFPHE 600  
Qy 510 ----- 509  
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGIADAVIADGINHDVTTAWGGDY 660  
Qy 510 ----- 560  
Db 661 WRLLTPGDYMWVTASAGYHSVTRNCRTVTEEGFPFCNFVLTPTKPKORLRELLAAGAKVPP 720  
Qy 561 DLRRLRLRGQKD 574  
Db 721 DLRRLRLRGQKD 734

RESULT 11  
US-09-813-432-38  
; Sequence 38, Application US/09813432  
; Publication No. US20030148485A1  
; GENERAL INFORMATION:  
; APPLICANT: Taupier Jr., Raymond J  
; APPLICANT: Majmuder, Kamud  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Vernet, Corine A. M.  
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same  
; FILE REFERENCE: 15966-729  
; CURRENT APPLICATION NUMBER: US/09/813,432  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,835  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: 60/190,768  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: 60/190,972  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/191,199  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/191,947  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,665  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,657  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,984  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,664  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,836  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/193,843  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 734  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-432-38

Query Match 96.9%; Score 2976; DB 10; Length 734;  
Best Local Similarity 78.1%; Pred. No. 4.9e-251;  
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAPAPAVGALGAPNSVLGLAQPGTTKVPGSTPALHSSPAOPPAETANGTS 60  
Db 1 MWGLLLAALAPAVGALGAPNSVLGLAQPGTTKVPGSTPALHSSPAOPPAETANGTS 60  
Qy 61 EQHVRIRVITKKKVIWKRRKKLTLTRPTPLVATAGPLVTPAGTLPDPAEQETGCPPLGL 120  
Db 61 EQHVRIRVITKKKVIWKRRKKLTLTRPTPLVATAGPLVTPAGTLPDPAEQETGCPPLGL 120  
Qy 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNIQSGLEDGDLYDGAWCABEQDADPWFQVDAGH 180  
Db 121 ESLRVSDSRLEASSSOSFGLGPHRGRNLNIQSGLEDGDLYDGAWCABEQDADPWFQVDAGH 180  
Qy 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
Db 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
Qy 241 NLLPEQVAPRIRLLPQTWLGQAPCLRAEILACPVSDDPNDLFLLEAPASGSSDPLDFQHH 300  
Db 241 NLLPEQVAPRIRLLPQTWLGQAPCLRAEILACPVSDDPNDLFLLEAPASGSSDPLDFQHH 300  
Qy 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGCEHELGEPEVRYVAGMH 360  
Db 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGCEHELGEPEVRYVAGMH 360  
Qy 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
Db 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDCGYEYAYHRGSELVG 420  
Qy 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPYHIVPNHHLPLPTYTYTLPNATVAPETR 480  
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPYHIVPNHHLPLPTYTYTLPNATVAPETR 480  
Qy 481 AVIKMKRKIPFVLSANLHGELVVSYPFD----- 509  
Db 481 AVIKMKRKIPFVLSANLHGELVVSYPFD----- 540  
Qy 510 ----- 509  
Db 541 LAMQDTSRRPCHSQDPSVHGNIINGADWHTVPGSMNDFSYLHTNCPVTVVELSCDKFPHE 600  
Qy 510 ----- 509  
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGIADAVIADGINHDVTTAWGGDY 660  
Qy 510 ----- 560  
Db 661 WRLLTPGDYMWVTASAGYHSVTRNCRTVTEEGFPFCNFVLTPTKPKORLRELLAAGAKVPP 720  
Qy 561 DLRRLRLRGQKD 574  
Db 721 DLRRLRLRGQKD 734

RESULT 12  
US-10-174-364-38  
; Sequence 38, Application US/10174364  
; Publication No. US20030216308A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson et al.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-729CIP2  
; CURRENT APPLICATION NUMBER: US/10/174,364



241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAPASGSSDPLDFQHH 300  
241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAPASGSSDPLDFQHH 300  
301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYOGLKLYWEMSDKPEGEHELGEPEVRYVAGMH 360  
301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYOGLKLYWEMSDKPEGEHELGEPEVRYVAGMH 360  
361 GNEALGRELILLMLQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPQGYEYAYHRGSELVG 420  
361 GNEALGRELILLMLQFLCHEFLRGNQVTRLLSEMRIHLLPSMNPQGYEYAYHRGSELVG 420  
421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPTYYTLPNATVAPETR 480  
421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPTYYTLPNATVAPETR 480  
481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509  
481 AVIKMKRIPFVLSANLHGELVVSYPFDWTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540  
510 ----- 509  
541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSILHTNCFEVTVELSCDKFPHE 600  
510 ----- 509  
601 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSILHTNCFEVTVELSCDKFPHE 660  
510 ----- 509  
661 WRLLTPGDYMTASAGYHSVTRNCRVTPBEGFPFCNFVLTTPKQRLRELLAAGAKVPP 720  
561 DLRRRLRLRGQKD 574  
721 DLRRRLRLRGQKD 734

RESULT 14  
US-10-689-832-38  
; Sequence 38, Application US/10689832  
; Publication No. US20040121380A1  
; GENERAL INFORMATION:  
; APPLICANT: Majmuder, Kamud  
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same  
; FILE REFERENCE: 15966-729DIV1  
; CURRENT APPLICATION NUMBER: US/10/689, 832  
; CURRENT FILING DATE: 2003-10-20  
; PRIOR APPLICATION NUMBER: 09/813,432  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,835  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: 60/190,768  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: 60/190,972  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/191,199  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/191,947  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,665  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,657  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,984  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 60/192,664  
; PRIOR FILING DATE: 2000-03-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 734  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-689-832-38  
Query Match 96.9%; Score 2976; DB 16; Length 734;  
Best Local Similarity 78.1%; Pred. No. 4.9e-251;  
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;  
QY 1 MGLLLALAAFAVPAVGALGAPRNSVLGLAQPGCTTKVPGSTPALHSSPAQPAETANGTS 60  
DB 1 MGLLLALAAFAVPAVGALGAPRNSVLGLAQPGCTTKVPGSTPALHSSPAQPAETANGTS 60  
QY 61 EQHVRIRVIXKKKVIKKKXKLLTRPTPLVITAGPLVITPAGTLPDAEKQETGCPPLGL 120  
DB 61 EQHVRIRVIXKKKVIKKKXKLLTRPTPLVITAGPLVITPAGTLPDAEKQETGCPPLGL 120  
QY 121 ESLRVSDSLSEASSOSFGLGPHRGRLNIQSGLDGLYDGAWCAEQDADPMFQVDAGH 180  
DB 121 ESLRVSDSLSEASSOSFGLGPHRGRLNIQSGLDGLYDGAWCAEQDADPMFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVMRYDWVITSYKVQFSNDSRTWMSRNHSSGMDAVFPANSDPETPVL 240  
DB 181 PTRFSGVITQGRNSVMRYDWVITSYKVQFSNDSRTWMSRNHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAPASGSSDPLDFQHH 300  
DB 241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAPASGSSDPLDFQHH 300  
QY 301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYOGLKLYWEMSDKPEGEHELGEPEVRYVAGMH 360  
DB 301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYOGLKLYWEMSDKPEGEHELGEPEVRYVAGMH 360  
QY 361 GNEALGRELILLMLQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPQGYEYAYHRGSELVG 420  
DB 361 GNEALGRELILLMLQFLCHEFLRGNQVTRLLSEMRIHLLPSMNPQGYEYAYHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPTYYTLPNATVAPETR 480  
DB 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDQGVPHIVPNHHLPLPTYYTLPNATVAPETR 480  
QY 481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509  
DB 481 AVIKMKRIPFVLSANLHGELVVSYPFDWTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540  
QY 510 ----- 509  
DB 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSILHTNCFEVTVELSCDKFPHE 600  
QY 510 ----- 509  
DB 601 NELPQWENNKDALLTYLEQVRMGIAGVVRDKDTLGIADAVIADVGINHDTVWGGDY 660  
QY 510 ----- 509  
DB 661 WRLLTPGDYMTASAGYHSVTRNCRVTPBEGFPFCNFVLTTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
DB 721 DLRRRLRLRGQKD 734

RESULT 15  
US-10-052-586-458  
; Sequence 458, Application US/10052586  
; Publication No. US20020127584A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C1  
; CURRENT APPLICATION NUMBER: US/10/052,586  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
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; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
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; PRIOR FILING DATE: 1997-10-31  
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; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
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; PRIOR APPLICATION NUMBER: 60/069425  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: 60/069870  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/068017  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
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; PRIOR FILING DATE: 1998-03-11  
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; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081049  
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; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/086392  
; PRIOR FILING DATE: 1998-05-22  
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; PRIOR FILING DATE: 1998-05-22  
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; PRIOR APPLICATION NUMBER: 60/087208  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087609  
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; PRIOR APPLICATION NUMBER: 60/087759  
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; PRIOR FILING DATE: 1998-06-03  
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; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088033  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088167  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/088202  
; PRIOR FILING DATE: 1998-06-05





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 19:28:10 ; Search time 43 Seconds  
(without alignments)  
1284.382 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLALAAFAFAPVGPALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1166	38.0	845	2 JC5256	adipocyte transcri
2	1071.5	34.9	719	2 S51739	transcription repr
3	616	20.1	458	2 S02074	lysine carboxypept
4	582.5	19.0	454	2 A54324	carboxypeptidase H
5	579	18.9	476	2 S12461	carboxypeptidase E
6	579	18.9	476	2 A40469	carboxypeptidase E
7	574	18.7	476	2 S09489	carboxypeptidase E
8	564	18.4	448	2 A24327	carboxypeptidase E
9	563.5	18.4	477	2 S16383	carboxypeptidase E
10	495.5	16.1	1389	2 I50090	carboxypeptidase g
11	458.5	14.9	1446	2 T30916	carboxypeptidase D
12	439.5	14.3	1119	2 T13284	carboxypeptidase (
13	439.5	14.3	1404	2 T13420	probable carboxype
14	439.5	14.3	1406	2 T13421	probable carboxype
15	431	14.0	472	2 T20454	hypothetical prote
16	415	13.5	985	2 T29910	hypothetical prote
17	402.5	13.1	439	2 A32619	carboxypeptidase M
18	400.5	13.0	501	2 T25343	hypothetical prote
19	351	11.4	491	2 B96739	hypothetical prote
20	252.5	8.2	218	2 A47285	milk fat globule p
21	249	8.1	427	2 JC4915	ags protein precu
22	248	8.1	463	1 A36479	milk fat globule m
23	236.5	7.7	2183	2 T42764	coagulation factor
24	229.5	7.5	2211	1 KFB05	coagulation factor
25	227	7.4	409	2 T11743	pp47 protein - pig
26	224.5	7.3	2224	1 KFHU5	coagulation factor
27	224	7.3	2133	2 T42763	coagulation factor
28	221	7.2	401	2 S65138	glycoprotein antig
29	221	7.2	427	2 S74211	PAS-6/7 protein pr

factor VIII-associ  
coagulation factor  
coagulation factor  
carboxypeptidase T  
probable zinc-bind  
receptor tyrosine k  
protein-tyrosine k  
A5 antigen precurs  
carboxypeptidase (

ALIGNMENTS

RESULT 1

JC5256

adipocyte transcription factor, ABBP1 - human

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C/Accession: JC5256

R/Ohno, I.; Hashimoto, J.; Shimizu, K.; Takaoka, K.; Ochi, T.; Matsubara, K.; Okubo, K.

Biochem. Biophys. Res. Commun. 228, 411-414, 1996

A/Title: A cDNA cloning of human ABBP1 from primary cultured osteoblasts and its express

A/Reference number: JC5256; MUID:97079196; PMID:8920928

A/Accession: JC5256

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-845 <OHN>

A/Cross-references: UNIPROT:Q14113; DBJ:D86479; NID:g1468942; PIDN:BAA13094.1; PID:g146

Query Match 38.0%; Score 1166; DB 2; Length 845;

Best Local Similarity 37.7%; Pred. No. 6.9e-80;

Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8;

Qy	107	PASQETGCPPLGLESRLVSDSRLEASSQSFGLGPHRGRLNTQSGLEDGLYDGAWCAE	166
Db	66	PTEKVK--CPPIGWESHRIEDNQIRASSMLRHGLGAQRGLNMQTGATEDDYDGAWCAE	123
Qy	167	EQADAPKFOVDAGHPTREFSGVITQGSNVRYDMVTSYKVOFNSDSTWGSRNHSSGMD	226
Db	124	DDARTQWIEVDTRTRTRFTGVIITQGRDSSIHDDFVTTFVFGFNSDSQTVMYNTNGYSEM-	182
Qy	227	AVFPANSDPPTPVNLILLPEQVAFRILLPQTWLGQGAPCLRAEILACVPVSDPNDLFLEA	286
Db	183	-TFHGNVDKDTPLVSELPEPVAFRIYPLTW--NGSLCMRLEVLCGSVAPVYSYAQN	239
Qy	287	PASGSDPLDFQHHNYKAMRKLKMQVOEQCPNTRIYSICKSYQGLKLYWMSDKPGEH	346
Db	240	EVV-ATDDLDFRHHSYKDMRQLMKVNEECPTITRTYSLGSKSRGLKIYAMEISDNPGEH	298
Qy	347	ELGEPEVRYVACGMHGENLGRILLMLLOFLCHEFLRGNPRVTRLISEMHIHLLPSMNP	406
Db	299	ELGEPEFRYTAGTHGNEVLGRELMLLMQYLCHREYRDGNPRVRSLVQDTRIHLVPSLNPD	358
Qy	407	GVBIAVHRGSELVGAEGRWNNQSIDLNNHFNADLNTPLWEAODDGKVPHTVPNNHLLPLPT	466
Db	359	GYEVAQMSEFGNWLGLWTESGFDIFEDPDLNSVLWGAERKWKVPYRVPNNLLPIPE	418
Qy	467	YITLPNATVAPETRAVIKMKRIPFVLISANLHGELVVSYPFDM-----	510
Db	419	RYLSPDATVSTEVRAIIAWMEKNPFVLGNLNGERLVSYPYDMARTPTQQLAAAMAA	478
Qy	511	-----	510
Db	479	ARGEDEVESEAQETPDHAFIRWLAIASFASAHLLTLEPYRGCGCAQDYTGGMGVNGAKW	538

QY 511 ----- 510  
Db 539 NPRTGTINDFSYLHTNCLSELSFYLGCDFPHESELPREWENNKALLTFMEQVHRGKGV 598  
QY 511 -----VTASAEGYHVSVTRCRVTF 529  
Db 599 VTDEQGIPIANATISVSGINHGKVTASGGDYWRIILNPGCYRVTAHAEGYTPSAKTCNDY 658  
QY 530 EGGPPCNFVLTQKQRLRELLAAGKVP-----PDLR-----RLRG 571  
Db 659 DIGATQCNCFILARSWKIREIMAMNGNRPIPHIDPSRPMPQQORRLQRLRLRA 718  
QY 572 Q 572  
Db 719 Q 719

RESULT 2  
S51739  
transcription repressor AEBP1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
A:Accession: S60227; S51739  
R:He, G.P.; Muise, A.; Li, A.W.; Ro, H.S.  
Nature 378, 92-96, 1995  
A:Title: A eukaryotic transcriptional repressor with carboxypeptidase activity.  
A:Reference number: S60227; PMID:96061010; PMID:7477299  
A:Accession: S60227  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-719 <HE2>  
A:Cross-references: UNIPROT:Q61281; EMBL:X80478; NID:g607131; PIDN:CAA56648.1; PID:g6071

Query Match 34.98; Score 1071.5; DB 2; Length 719;  
Best Local Similarity 36.8%; Pred. No. 7.Se-73;  
Matches 224; Conservative 68; Mismatches 123; Indels 193; Gaps 5;

QY 149 IQSGLEDGDIYDGAWCAEEQDAPFWQVDAGHPTFRFSGVITQGRNSVMRYDWVTSYKVQF 208  
Db 1 MQAGANEDDYDGAWCAEDSDSQWIEVDTRRTFTGTGVTQGRDSIHDDFTFFVQF 60  
QY 209 SNDSTRWGRNHSNGDVAFPANSDPTVLNLLPEQVAFIRLLPOTVLQGGAPCLR 268  
Db 61 SNDSTQWMTVNGYEEM--TFYGNVDKDTPLSELPEPVVAFIRIYPLTW--NGSLCNR 116  
QY 269 AEILACPVSDDNDFLEAPASGSSDPLDFOHNYKAMRKLKMQVQOCQCNITRIYSIGS 328  
Db 117 LEVLGCPVTPVSYAQNEVV--TTDSLDFRHSYKDMRQMKAVNEECFTIIRTSYLGKS 175  
QY 329 YQGLKLYVMEMSKPGHEHGEPEVRYVAGMHGNEALGRELLLLMQFLCHEFLRGNPRV 388  
Db 176 SRGLKIYAMEISDNPGDHGEPEFRYTAGIHGNEVLGRELLLLMQVLCQEVYRDNPRV 235  
QY 389 TRLLSEMRHLLPSMNPDCGYETAYHRGSELVGAEGRWNNQSIDLNHNPDINTPLWEAQ 448  
Db 236 RNUQDTRHLVPSLNPDPGYEAAQMGSEFGNWLGLWTEEGFDIFEDFPDLNSVLAAE 295  
QY 449 DQKVPVHVPNHHPLPFTYITPNATVAPETRAVTKMKRIPFVLSANLHGELVVSYPF 508  
Db 296 EKKWVYRVFNNLPIPERYLPDQVSTVEVRAISWMEKNFVLSANLHGELVVSYPY 355  
QY 509 DM----- 510  
Db 356 DMARTSPQQLAEALAAARGDDGVSQAQETPDHAFIRWLAISFASAHLTMTPEYRG 415  
QY 511 ----- 510  
Db 416 CQAQDYTCGIVNGAKWNPSTGTFNDRSYLHTNCLSELSVYLGCDKFFHESELPREWENN 475  
QY 511 -----V 511  
Db 476 KEALLTFMEQVHRGKGVVTDQGIPIANATISVSGINHGKVTASGGDYWRIILNPGCYRV 535

QY 512 TASAEGYHVSVTRCRVTFEEGPPCNFVLTQKQRLRELLAAGKVP-----P 560  
Db 536 TAAHAGYTSKATCNVDYDIGATQCNCFILARSWKIREILLAMNGNRPIRLRVDPSPRPMT 595  
QY 561 DLRRLER 568  
Db 596 QQRMQQR 603

RESULT 3  
S02074

lysine carboxypeptidase (EC 3.4.17.3) small chain precursor - human

N:Alternate names: anaphylatoxin inactivator small subunit; carboxypeptidase N small subunit

C:Species: Homo sapiens (man)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

A:Accession: S02074

R:Gebhard, W.; Schube, M.; Eulitz, M.

Eur. J. Biochem. 178, 603-607, 1989

A:Title: cDNA cloning and complete primary structure of the small, active subunit of human

A:Reference number: S02074; PMID:89107181; PMID:2912725

A:Accession: S02074

A:Molecule type: mRNA

A:Residues: 1-458 &lt;GEB&gt;

A:Cross-references: UNIPROT:P15169; EMBL:X14329; NID:g30296; PIDN:CAA32507.1; PID:g30297

A:Note: part of this sequence, including the amino end of the mature protein, was confirm

C:Superfamily: human carboxypeptidase H

C:Keywords: hydrolase; metallo-carboxypeptidase

F:1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F:21-458/Product: lysine (arginine) carboxypeptidase small chain #status experimental &lt;M

Query Match 20.1%; Score 616; DB 2; Length 458;  
Best Local Similarity 48.1%; Pred. No. 1e-38;  
Matches 125; Conservative 36; Mismatches 75; Indels 24; Gaps 4;

QY 294 PLDFOHNYKAMRKLKMQVQOCQCNITRIYSIGSKYQGLKLYVMEMSKPGHEHGEPEV 353  
Db 20 PVTFRHHYDDLVRLLKLVQNECGITRVYSIGSRVGRHLVLEFSDHPCHEFLPEV 79  
QY 354 RYVAGMHGNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNPDCGYETAYH 413  
Db 80 KYVGNMGHNEALGRELLMLQSEFLCEFRNRNORIVQLQDTRIHILPSMNPDCGYEVAAA 139  
QY 414 RGSSELVGAEGRWNNQSIDLNHNPDINTPLWEAQDDQKVPVHVPNHHPLPPTYITLPA 473  
Db 140 QGPNKPGYLVGRNNAVGVLDNRNPPDNTYIYNEKYGG-----PNHLLPLPDNW---KS 191  
QY 474 TVAPETRAVTKMKRIPFVLSANLHGELVVSYPFDMVTASABGYHSVTRNCRVTFEEGP 533  
Db 192 QVEPETRAVIRWMHSEFNFLSANLHGGAVVANYPD-----KSPFHRVGVGVRT----- 240  
QY 534 FPCNFVLTQKQRLRELLA 553  
Db 241 -----ASTPTPDDKLFQKLA 255

RESULT 4  
A54324

carboxypeptidase H - American goosefish

C:Species: Lophius americanus (American goosefish)

C:Date: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

A:Accession: A54324

R:Roth, W.W.; Macklin, R.B.; Spies, J.; Goodman, R.H.; Noe, B.D.

Mol. Cell. Endocrinol. 78, 171-178, 1991

A:Title: Primary structure and tissue distribution of anglerfish carboxypeptidase H.

A:Reference number: A54324; PMID:92137483; PMID:1778303

A:Accession: A54324

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-454 &lt;ROT&gt;

A:Cross-references: UNIPROT:P37892; GB:S80565; NID:g244402; PIDN:AAA03252.1; PID:g244403

A:Note: sequence extracted from NCBI backbone (NCBI:80565, NCBI:80566)

C:Superfamily: human carboxypeptidase H





Db 207 PNNHL-LKNLKKIVDQNSKLAPETKAVIHWIMDIPFVLSANLHGGDLVANYPYDETRSGT 265  
Qy 515 AEGYHS 520  
Db 266 AHEYSS 271  
RESULT 10  
I50090  
carboxypeptidase gp180 - Anas sp.  
C;Species: Anas sp.  
C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: I50090  
R;Kuroki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.  
J. Biol. Chem. 270, 15022-15028, 1995  
A;Title: gp180, a host cell glycoprotein that binds duck hepatitis B virus particles, is  
A;Reference number: A57010; MUID:95318059; PMID:17797483  
A;Accession: I50090  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1389 <KUR>  
A;Cross-references: UNIPROT:Q90240; EMBL:U25126; NID:g1008477; PIDN:AAA78903.1; PID:g1008477  
Query Match 16.1%; Score 495.5; DB 2; Length 1389;  
Best Local Similarity 31.1%; Pred. No. 6.5e-29;  
Matches 133; Conservative 60; Mismatches 112; Indels 123; Gaps 18;  
Qy 154 EDGDLV-DGAWCAEQADPWFQVDAGHPTFRFSVITQGRNSVWRVYDWVTSYKVPQ---- 208  
Db 315 EREGTFQDGI-----TNGAQMVDVEGMDQ-----YNYVMANCFEITLSC 356  
Qy 209 -----SNDSTRWMSGRNHS-----SGM--DAVFPANSDPTETPVL-----NLLPE 245  
Db 357 CKYPTSELQOEWNRESLLTFIEKVHIGVKGFVRDAITGAGLENATIVVAGIAHNITA 416  
Qy 246 PQVAFIRLL-PQW-----LQGAFCRLAEI-----LACPVSDDN-D 281  
Db 417 GKFGDYHRLVPGTYNVTAVMGVAPYTKENIEVKEADATVDFSLQTPVAP--DNLTL 474  
Qy 282 LLEAPASGSS-----DPLDFOHNYKAMKMLKMQVQOCNPITR 321  
Db 475 QFTATPAPPSTLTFSAQVPEPPATTSLHQAVQVPDFRHHFSDMEIFLRRYANEYSITR 534  
Qy 322 IYSIGKSYQGLKLYVMEMSDKPGHELGEPVRYVAGHNEALGRELLLLMQFLCHEF 381  
Db 535 LYSVGKSVLELYVWEISNPGIHEAGEPEFKYIGNHGHNEVVGRELLLNLEYLCKNP 594  
Qy 382 LRGNPRVTRLSEMIRHLLPSMNPDPGYEIAHYRGSELVWAGRWNNQSIDLNNHFNADLN 441  
Db 595 -GTDPEVTDLVQSTRIHMPSMNPDGYEKS-QEGDR--GGTVGRNNSNYDLNRNFPD-- 648  
Qy 442 TPLWEAQDDGKVPHIVPNHLLPLPTYYTLPNATVAPETRAVIKMKRIPFVLSANLHGGE 501  
Db 649 -QFFQVTDPPQ-----PETLAVMWSLKTYPFVLSANLHGGSS 683  
Qy 502 LVVSYPPD 509  
Db 684 LVVNYPPD 691  
RESULT 11  
T30916  
carboxypeptidase D (EC 3.4.17.-) - California sea hare  
C;Species: Aplysia californica (California sea hare)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30916  
R;Fan, X.; Qian, Y.; Fricker, L.D.; Akatal, D.B.; Nagle, G.T.  
DNA Cell Biol. 18, 121-132, 1999  
A;Title: Cloning and expression of Aplysia carboxypeptidase D, a candidate prohormone-  
A;Reference number: Z20933; MUID:99171579; PMID:10073571  
A;Accession: T30916  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-1446 <FAN>  
A;Cross-references: UNIPROT:O77063; EMBL:AF007570; NID:g3642735; PID:g3642736; PIDN:AAC3.  
C;Keywords: hydrolase; metallo-carboxypeptidase  
Query Match 14.9%; Score 458.5; DB 2; Length 1446;  
Best Local Similarity 38.1%; Pred. No. 4.3e-26;  
Matches 96; Conservative 46; Mismatches 65; Indels 45; Gaps 6;  
Qy 271 ILACPVSDDPNDL-----FLEAPASGSSDPLDFOHNYKAMKMLKMQVQOCNPIT 320  
Db 430 VVTVPGEPLDRLMSYLDGLKDFSHHSSTHFKEPSEFVHNFOEMTKFQQLADKYPALA 489  
Qy 321 RIYSIGKSYQGLKLYVMEMSDKPGHELGEPVRYVAGHNEALGRELLLLMQFLCHE 380  
Db 490 KLTISIGSVQGRDLWLVEITENFGQHPGKPEFKYIGNHGHNEVVGRELLLLAQLLCEN 549  
Qy 381 FLGNPRVTRLSEMIRHLLPSMNPDPGYEIAHYRGSELVWAGRWNNQSIDLNNHFNAD 439  
Db 550 YGQ--DDLVTLMQLQOTRVHIMPSPNPDGYE----KREGDVSGIRGRANANLVDLNRNFP 604  
Qy 440 L--NTPLWEAQDDGKVPHIVPNHLLPLPTYYTLPNATVAPETRAVIKMKRIPFVLSANL 497  
Db 605 LFHTSVNERQE-----PETLAVMRWSRSLPFVLSANL 637  
Qy 498 HGGELVVSYPPD 509  
Db 638 HGGSLVANYPPD 649  
RESULT 12  
T13284  
carboxypeptidase (EC 3.4.17.-) precursor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
C;Accession: T13284  
R;Settle, S.H.; Green, M.M.; Burtis, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9470-9474, 1995  
A;Title: The silver gene of Drosophila melanogaster encodes multiple carboxypeptidases  
A;Reference number: Z17649; MUID:96003800; PMID:7568156  
A;Accession: T13284  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1119 <SET>  
A;Cross-references: EMBL:U29591; NID:g974552; PID:g974553; PIDN:AAA91650.1  
A;Gene: svr  
A;Cross-references: FlyBase:FBgn0004648  
A;Map position: X  
C;Keywords: hydrolase; metallo-carboxypeptidase  
Query Match 14.3%; Score 439.5; DB 2; Length 1119;  
Best Local Similarity 42.1%; Pred. No. 8.1e-25;  
Matches 96; Conservative 31; Mismatches 68; Indels 33; Gaps 6;  
Qy 284 LLEAPASGSSDPLDFOHNYKAMKMLKMQVQOCNPITRIYSIGKSYQGLKLYVMEMSDKP 343  
Db 441 LKQFNGFLTPTKYEHNFNTAMESYLRAISSYPSLTRLSYIGKSVQGRDLWLVEIFATP 500  
Qy 344 GEHELGEPEVRYVAGHNEALGRELLLLMQFLCHEFIRGN--PRVTRLSEMRHLLPS 402  
Db 501 GSHVPGVPPEFKYVANNHGHNEVVGKELLILTKYMLERY--GNDRITKLVNTRMHFLYS 558  
Qy 403 MNPDPGYEIAHYRGSELVWAGRWNNQSIDLNNHFNADLTPLWEAQDDGKVPHIVPNHLL 462  
Db 559 MNPDPGYEISL-EGDRTGG--VGRANAHGIDLNRNFPD----- 592  
Qy 463 PLPTYTYT-LPNATVAPETRAVIKMKRIPFVLSANLHGGEVVSYPFD 509  
Db 593 ---QYGTDFNKTVEEVAAMVNWTLSPFVLSANLHGGSLVANYPPD 637  
RESULT 13

## Tl3420

probable carboxypeptidase (EC 3.4.17.-) - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: Tl3420  
R:Madueno, E.; de Pablo, B.; Modolell, J.  
submitted to the EMBL Data Library, April 1999  
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A:Reference number: Z17669

A:Accession: Tl3420

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1406 &lt;MAD&gt;

A:Cross-references: UNIPROT:P42787; EMBL:AL009147; NID:el314051; PID:el248570; PIDN:CAAL

C:Genetics:

A:Cross-references: FlyBase:FBgn0023535

A:Introns: 150/3; 229/2; 389/2; 423/1; 462/2; 904/3; 979/2

A&gt;Note: EG:17D11.3

C:Keywords: hydrolase; metallo-carboxypeptidase

Query Match 14.3%; Score 439.5; DB 2; Length 1404;  
Best Local Similarity 42.1%; Pred. No. 1.1e-24;  
Matches 96; Conservative 31; Mismatches 68; Indels 33; Gaps 6;

QY 284 LEAPASGSDPLDFOHNNYKAMKLMQVQECNPITRIYSIGKSYQGLKLYVMEMSDKP 343

DB 439 LKKQFNGFLTPTKYEHHNFTAMESYLRAISSSYPSLRLYSIGKSVQGRDLVWLEIFATP 498

QY 344 GHELGEPEVRVYVAGMHGNEALGRELILLMQFLCHEFLRGN-PRVTRLLSEMRHLLPS 402

DB 499 GSHVGVPEFKYVAMHGVVGGKELLILTKYMLERY--GNDDRITKLVNGTRMHFLYS 556

QY 403 MNPDGYEIAHRSSELVGAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPVHNHLL 462

DB 557 MNPDGYEISI-EGDRTGG--VGRANAHGIDLNRNFPD----- 590

QY 463 PLPTYYT-LPNATVAPETRAVIKMKRIPFVLSANLHGGSLVSYPPD 509

DB 591 ---QYGTDRFNKVTPEVAAMVNNWTLSPFVLSANLHGGSLVANYPPD 635

## RESULT 14

## Tl3421

probable carboxypeptidase (EC 3.4.17.-) - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: Tl3421

R:Madueno, E.; de Pablo, B.; Modolell, J.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17669

A:Accession: Tl3421

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1406 &lt;MAD&gt;

A:Cross-references: UNIPROT:P42787; EMBL:AL009147; NID:el314051; PID:el248569; PIDN:CAAL

C:Genetics:

A:Gene: FlyBase:avr

A:Cross-references: FlyBase:FBgn0004648

A:Introns: 152/3; 231/2; 391/2; 425/1; 464/2; 906/3; 981/2

C:Keywords: hydrolase; metallo-carboxypeptidase

Query Match 14.3%; Score 439.5; DB 2; Length 1406;  
Best Local Similarity 42.1%; Pred. No. 1.1e-24;  
Matches 96; Conservative 31; Mismatches 68; Indels 33; Gaps 6;

QY 284 LEAPASGSDPLDFOHNNYKAMKLMQVQECNPITRIYSIGKSYQGLKLYVMEMSDKP 343

DB 441 LKKQFNGFLTPTKYEHHNFTAMESYLRAISSSYPSLRLYSIGKSVQGRDLVWLEIFATP 500

QY 344 GHELGEPEVRVYVAGMHGNEALGRELILLMQFLCHEFLRGN-PRVTRLLSEMRHLLPS 402

DB 501 GSHVGVPEFKYVAMHGVVGGKELLILTKYMLERY--GNDDRITKLVNGTRMHFLYS 558

QY 403 MNPDGYEIAHRSSELVGAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPVHNHLL 462

DB 559 MNPDGYEISI-EGDRTGG--VGRANAHGIDLNRNFPD----- 592

QY 463 PLPTYYT-LPNATVAPETRAVIKMKRIPFVLSANLHGGSLVSYPPD 509

DB 593 ---QYGTDRFNKVTPEVAAMVNNWTLSPFVLSANLHGGSLVANYPPD 637

## RESULT 15

## T20454

hypothetical protein F01D4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T20454

R:Wild, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19278

A:Accession: T20454

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-472 &lt;WIL&gt;

A:Cross-references: UNIPROT:O17754; EMBL:Z81054; PIDN:CAB02881.1; GSPDB:GN00022; CESP:F01

A:Experimental source: clone F01D4

C:Genetics:

A:Gene: CESP:F01D4.4

A:Map position: 4

A:Introns: 59/3; 127/3; 334/3; 455/3

C:Superfamily: human carboxypeptidase H

Query Match 14.0%; Score 431; DB 2; Length 472;  
Best Local Similarity 42.0%; Pred. No. 1e-24;  
Matches 94; Conservative 37; Mismatches 83; Indels 10; Gaps 5;

QY 289 SGSS--DPLDFQH-HNYKAMKLMQVQECNPITRIYSIGKSYQGLKLYVMEMSDKPG 345

DB 27 SGSTHKDDAEWGHVHNNQALKEALKEINEKCPETITLYEIGQSVGEGRPLVVIQSTTPG 86

QY 346 HELGEPEVRVYVAGMHGNEALGRELILLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNP 405

DB 87 HIPTKPEVKLIGNMHGNEPIGRELLARFAETLCNGAINNDKEIVQLNSTSIHLFSMNP 146

QY 406 DGYEIAHRSSELVGAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPVHNHLLPLP 465

DB 147 DGFELALGTPEAQRQWLTCGRSNGVLDNRDPDLDSIFYELQKIG-VPKF--DHLLSL- 202

QY 466 TYTTLNATVAPETRAVIKMKRIPFVLSANLHGGSLVSYPPD 509

DB 203 ---FEDNVDROPETIAGQWTLSPFVLSANFEGDLVANYPPD 243

Search completed: January 10, 2005, 19:38:09

Job time : 46 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:20:10 ; Search time 198 Seconds

(without alignments)  
1668.005 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLALAAFAVAVGALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2975	96.9	734	2 Q6UW65	Q6UW65 homo sapien
2	2975	96.9	734	2 AAQ89315	AAQ89315 homo sapi
3	2974	96.9	734	2 O6P4G8	O6P4G8 homo sapien
4	2974	96.9	734	2 AAH63430	AAH63430 homo sapi
5	2972	96.8	734	1 CPXM HUMAN	Q36sm3 homo sapien
6	2491	81.1	477	2 Q8N2E1	Q8N2E1 homo sapien
7	2378.5	77.5	722	1 CPXM MOUSE	Q92l00 mus musculu
8	1400.5	45.6	764	1 CPX2 MOUSE	Q9d215 mus musculu
9	1390.5	45.3	756	1 CPX2 HUMAN	Q8n436 homo sapien
10	1357	44.2	430	2 Q8N2F1	Q8N2F1 homo sapien
11	1180.5	38.5	1128	2 Q88442	Q88442 mus musculu
12	1166	38.0	845	2 Q7KZ79	Q7KZ79 homo sapien
13	1166	38.0	1158	2 Q14113	Q14113 homo sapien
14	1166	38.0	1158	2 Q81UX7	Q81UX7 homo sapien
15	1073	35.0	728	2 Q97567	Q97567 bos taurus
16	1071.5	34.9	719	2 Q61281	Q61281 mus musculu
17	871	28.4	733	2 Q6ZSC7	Q6ZSC7 homo sapien
18	871	28.4	733	2 BAC87026	BAC87026 homo sapi
19	643.5	21.0	450	2 Q6N9Y4	Q6N9Y4 brachydanio
20	643.5	21.0	450	2 AAH66689	AAH66689 brachydan
21	628	20.5	652	2 O54858	O54858 rattus norv
22	628	20.5	652	2 O54859	O54859 rattus norv
23	624	20.3	654	2 Q8R4V4	Q8R4V4 mus musculu
24	616	20.1	458	1 CBPN HUMAN	P15169 homo sapien
25	613.5	20.0	453	2 Q6PAY9	Q6PAY9 xenopus lae
26	613.5	20.0	453	2 AAH59995	AAH59995 xenopus l
27	609	19.8	641	2 Q00520	Q00520 homo sapien
28	604	19.7	457	2 Q9JUN5	Q9JUN5 mus musculu
29	604	19.7	458	2 Q91WN9	Q91WN9 mus musculu
30	599	19.5	457	2 Q9EQV8	Q9EQV8 rattus norv
31	582.5	19.0	454	1 CBPE_LOPAM	P37892 lophius ame

32	579	18.9	476	1	CBPE_RAT	P15087 rattus norv
33	574	18.7	476	1	CBPE_HUMAN	P16870 homo sapien
34	572	18.6	476	1	CBPE_MOUSE	Q00493 mus musculu
35	572	18.6	476	2	BAC33184	BAC33184 mus muscu
36	566	18.4	454	2	Q6NSM5	Q6nsms brachydanio
37	566	18.4	454	2	AAH70026	AAH70026 brachydan
38	562.5	18.3	434	1	CBPE_BOVIN	P04836 bos taurus
39	556.5	18.1	647	2	Q8QGF3	Q8qgp3 gallus gall
40	511.5	16.7	1380	2	Q86XE6	Q86xe6 homo sapien
41	506.5	16.5	1380	1	CBPD_HUMAN	O75976 homo sapien
42	506.5	16.5	1380	2	Q86SH9	Q86sh9 homo sapien
43	502	16.4	1377	1	CBPD_MOUSE	Q89001 mus musculu
44	498.5	16.2	1133	2	Q9JHW1	Q9jhw1 rattus norv
45	498.5	16.2	1378	2	O35850	O35850 rattus norv

ALIGNMENTS

RESULT 1  
Q6UW65 PRELIMINARY; PRT; 734 AA.  
AC Q6UW65; 2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE CPXM.  
GN ORFNames=UNQ3015;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22897296; PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AY358956; AAQ89315.1; -;  
DR InterPro; IPR008969; CarboxypepD\_reg.  
DR InterPro; IPR000421; FA58 C.  
DR InterPro; IPR008979; Gal Bind like.  
DR InterPro; IPR000834; Peptidase\_M14.  
DR InterPro; IPR008575; Peptidase\_M14B.  
DR Pfam; PF00754; F5\_P8 type C; 1.  
DR Pfam; PF00246; Zn carboxypept; 1.  
DR PRINTS; PR00765; GRBOXYPTASEA.  
DR SMART; SM00231; FA58C; 1.  
DR SMART; SM00631; Zn pept; 1.  
DR PROSITE; PS00132; CARBOXYPEPT\_ZN\_1; 1.  
DR PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; 1.  
DR PROSITE; PS00022; FA58C\_3; 1.  
SQ SEQUENCE 734 AA; 81676 MW; B422FA5257301A38 CRC64;

Query Match 96.9%; Score 2975; DB 2; Length 734;  
Best Local Similarity 78.1%; Pred. No. 6.1e-209;  
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

Qy	1	MWGLLALAAFAVAVGALGAPRNSVLGAQPGTTKVPGSTPALHSSPAQPPAETANGTS	60
Db	1	MWGLLALAAFAVAVGALGAPRNSVLGAQPGTTKVPGSTPALHSSPAQPPAETANGTS	60

QY 61 EQHVRIRVKKKKVIMKKKKLTLTRPTPLVLTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
Db |||||  
QY 61 EQHVRIRVKKKKVIMKKKKLTLTRPTPLVLTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
Db |||||  
QY 121 ESLRVSDSLSEASSQSFGLGPHRGRLNIQSGLEDGLYDGAWCAEEQADPWFQVDAGH 180  
Db |||||  
QY 121 ESLRVSDSLSEASSQSFGLGPHRGRLNIHSGLEDGLYDGAWCAEEQADPWFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFSDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
Db |||||  
QY 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFSDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEPQVAFIRLLPQTLWGGAPCLRAEILACVSDPNDLFLFEPASGSSDPLDFQHH 300  
Db |||||  
QY 241 NLLPEPQVAFIRLLPQTLWGGAPCLRAEILACVSDPNDLFLFEPASGSSDPLDFQHH 300  
QY 301 NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360  
Db |||||  
QY 301 NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
Db |||||  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPKPHIVPNHHLPLPTYYTILPNATVAPETR 480  
Db |||||  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPKPHIVPNHHLPLPTYYTILPNATVAPETR 480  
QY 481 AVIKWMKRIPEVLSANLHGGLVVSYPFD 509  
Db |||||  
QY 481 AVIKWMKRIPEVLSANLHGGLVVSYPFD 509  
QY 510 510 509  
QY 541 LAMQDTSRRPCHSQDPSFHGNIINGADWHTVPGSMNDFSYLHTNCPEVTVELSCDKFPHE 600  
QY 510 510 509  
QY 601 NELPQEWNNKDALLTYLEQVRMGIAGVVRDKDTLGLADIADAVIADGINHDVTTANGDY 660  
QY 510 510 509  
QY 661 WRLTTPGDYMWVTSAGYHSVTRNCRTVEEGPPCNFVLTTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db |||||  
QY 721 DLRRRLRLRGQKD 734

## RESULT 2

AAQ89315 PRELIMINARY; PRT; 734 AA.  
AC AAQ89315;  
DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
DE CPXM  
DE UNQ3015.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Sestagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wiegand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;  
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
RT Bioinformatics Assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AY358956; AAQ89315.1; -.  
SQ SEQUENCE 734 AA; 81676 MW; B422FA5257301A38 CRC64;

Query Match 96.9%; Score 2975; DB 2; Length 734;  
Best Local Similarity 78.1%; Pred. No. 6.1e-209;  
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

QY 1 MGLLLALAAPAVGVPALGAPRNSVLGLAQPGITTKVFGSTPALHSSPAQPAETANGTS 60  
Db |||||  
QY 1 MGLLLALAAPAVGVPALGAPRNSVLGLAQPGITTKVFGSTPALHSSPAQPAETANGTS 60  
QY 61 EQHVRIRVKKKKVIMKKKKLTLTRPTPLVLTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
Db |||||  
QY 61 EQHVRIRVKKKKVIMKKKKLTLTRPTPLVLTAGLVTPPTAGTLDPAEKQETGCPPLGL 120  
QY 121 ESLRVSDSLSEASSQSFGLGPHRGRLNIQSGLEDGLYDGAWCAEEQADPWFQVDAGH 180  
Db |||||  
QY 121 ESLRVSDSLSEASSQSFGLGPHRGRLNIHSGLEDGLYDGAWCAEEQADPWFQVDAGH 180  
QY 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFSDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
Db |||||  
QY 181 PTRFSGVITQGRNSVWRDYDWTYSYKQFSDSRTWGSRNHSSGMDAVFPANSDPETPVL 240  
QY 241 NLLPEPQVAFIRLLPQTLWGGAPCLRAEILACVSDPNDLFLFEPASGSSDPLDFQHH 300  
Db |||||  
QY 241 NLLPEPQVAFIRLLPQTLWGGAPCLRAEILACVSDPNDLFLFEPASGSSDPLDFQHH 300  
QY 301 NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360  
Db |||||  
QY 301 NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
Db |||||  
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPKPHIVPNHHLPLPTYYTILPNATVAPETR 480  
Db |||||  
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPKPHIVPNHHLPLPTYYTILPNATVAPETR 480  
QY 481 AVIKWMKRIPEVLSANLHGGLVVSYPFD 509  
Db |||||  
QY 481 AVIKWMKRIPEVLSANLHGGLVVSYPFD 509  
QY 510 510 509  
QY 541 LAMQDTSRRPCHSQDPSFHGNIINGADWHTVPGSMNDFSYLHTNCPEVTVELSCDKFPHE 600  
QY 510 510 509  
QY 601 NELPQEWNNKDALLTYLEQVRMGIAGVVRDKDTLGLADIADAVIADGINHDVTTANGDY 660  
QY 510 510 509  
QY 661 WRLTTPGDYMWVTSAGYHSVTRNCRTVEEGPPCNFVLTTPKQRLRELLAAGAKVPP 720  
QY 561 DLRRRLRLRGQKD 574  
Db |||||  
QY 721 DLRRRLRLRGQKD 734

## RESULT 3

Q6P4G8  
ID Q6P4G8 PRELIMINARY; PRT; 734 AA.  
AC Q6P4G8;  
DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Metalloproteinase CPX-1.





SEQUENCE FROM N.A. (ISOFORM 2).

RP TISSUE=Embryonic brain;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J.J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4].

RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).

RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;

RA Hillman R.T., Green R.E., Brenner S.E.;

RT "An unappreciated role for RNA surveillance.";

RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).

CC -I- FUNCTION: May be involved in cell-cell interactions. No

CC carboxypeptidase activity was found yet (By similarity).

CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -I- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q96SM3-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q96SM3-2; Sequence=VSP\_000780, VSP\_000781;

CC Note=May be produced at very low levels due to a premature stop

CC codon in the mRNA, leading to nonsense-mediated mRNA decay. No

CC experimental confirmation available;

CC -I- SIMILARITY: Belongs to peptidase family M14.

CC -I- SIMILARITY: Contains 1 F5/8 type C domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>

CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

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DR EMBL; AK027661; BAB55275.1; -;

DR EMBL; AL035460; CAB2246.1; -;

DR EMBL; BC032692; AAH32692.1; -;

DR HSSP; Q90240; 1H8L.

DR MEROPS; M14.015; -;

DR Genew; HGNC:15771; CPXM.

DR InterPro; IPR008969; CarboxypepD\_reg.

DR InterPro; IPR000421; F58\_C.

DR InterPro; IPR008979; Gal\_Bind\_like.

DR InterPro; IPR000834; Peptidase\_M14.

DR InterPro; IPR008575; Peptidase\_M14B.

DR Pfam; PF05895; DUF857; 1.

DR Pfam; PF00754; F5\_F8\_type\_C; 1.

DR Pfam; PF00246; Zn\_carboxypept; 1.

DR PRINTS; PR00765; CRBOXYPTASEA.

DR SMART; SM00231; FA58C; 1.

DR SMART; SM00631; Zn\_dept; 1.

DR PROSITE; PS00132; CARBOXYPEPT\_ZN\_1; 1.

DR PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; 1.

DR PROSITE; PS01285; FA58C\_1; FALSE NEG.

DR PROSITE; PS01286; FA58C\_2; FALSE NEG.

DR PROSITE; PS50022; FA58C\_3; 1.

KW Alternative splicing; Carboxypeptidase; Glycoprotein; Hydrolase;

KW Metalloprotease; Signal; Zinc.

FT SIGNAL 1 20 Potential.

FT CHAIN 21 734 Potential carboxypeptidase X.

FT DOMAIN 113 274 F5/8 type C.

FT DOMAIN 70 73 Poly-Lys.

FT DOMAIN 369 373 Poly-Leu.

FT METAL 360 360 Zinc (By similarity).

FT METAL 363 363 Zinc (By similarity).

FT METAL 498 498 Zinc (By similarity).

FT ACT\_SITE 591 591 Nucleophile (By similarity).

FT DISULFID 115 274 By similarity.

FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 220 220 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 318 318 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 428 428 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 472 472 N-linked (GlcNAc...) (Potential).

FT VARSPLIC 308 356 LMKVQEQCPNITRIYSIGKSYQGLKLYMMSDKPGEHEL

FT GEPEVRV -> VRYNPYDILGRRAHPSQVFPFSPSHRGTTC

FT DCACMPLLPDVSFAFSQVDP (in isoform 2).

FT /FTId=VSP\_000780.

FT Missing (in isoform 2).

FT VARSPLIC 357 734 /FTId=VSP\_000781.

FT CONFLICT 390 390 W -> R (in Ref. 2).

FT SQ SEQUENCE 734 AA; 81697 MW; 815705578E9A58F3 CRC64;

Query Match 96.8%; Score 2972; DB 1; Length 734;

Best Local Similarity 78.1%; Pred. No. 1e-208; 1; Indels 160; Gaps 1;

Matches 573; Conservative 0; Mismatches 1;

QY 1 MWGLLLAALFAFAPAVGALCAPRNSVLGLAQPGCTTKVPGSTPALHSSPAOPPAETANGTS 60

DB 1 MWGLLLAALFAFAPAVGALCAPRNSVLGLAQPGCTTKVPGSTPALHSSPAOPPAETANGTS 60

QY 61 EQHVRIRVTKKKKVIIMKKRKKLTLRPTPLVITAGPLVITPAGTLPDAEKQETGCPPLGL 120

DB 61 EQHVRIRVTKKKKVIIMKKRKKLTLRPTPLVITAGPLVITPAGTLPDAEKQETGCPPLGL 120

QY 121 ESURVSDSRLEASSSSQFGLGPHRGRLNITQSGLEDGLYDVGACAEQDADPFQVDAGH 180

DB 121 ESURVSDSRLEASSSSQFGLGPHRGRLNITQSGLEDGLYDVGACAEQDADPFQVDAGH 180

QY 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWMSGRNHSMDAVFPANSDPETPVL 240

DB 181 PTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWMSGRNHSMDAVFPANSDPETPVL 240

QY 241 NULLPEQVARFIRLLPQTWLGQAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 300

DB 241 NULLPEQVARFIRLLPQTWLGQAPCLRAEILACPVSDPNDLPLEAPAGSSDPLDFQHH 300

QY 301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYQGLKLYMMSDKPGEHELCEPEVRYVAGMH 360

DB 301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYQGLKLYMMSDKPGEHELCEPEVRYVAGMH 360

QY 361 GNEALGRELLLLLMQFLCHEFLRGNGPRVTRLLSEMRHLLPSMNPQGYEIAHRSSELVG 420

DB 361 GNEALGRELLLLLMQFLCHEFLRGNGPRVTRLLSEMRHLLPSMNPQGYEIAHRSSELVG 420

QY 421 WAEGRWNNQSIDLNHNFNADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETR 480

DB 421 WAEGRWNNQSIDLNHNFNADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETR 480

QY 481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509

DB 481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509

QY 510 ----- 509

DB 541 LAMQDTSRRPCHQSDPSVHGNIINGADWTVPQSMNDFSYLHTNCFEVTVELSCDFPHE 600

QY 510 ----- 509

```

Db 601 NELPOWENNKDALLTYLEQVRMGAGVVRDKDTLGIADAVIADGINHDVTTANGGDY 660
Qy 510 -----MYTASAGVHSYTRNCRTFFBEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 560
Db 661 WRLTTPGDYMYTASAGVHSYTRNCRTFFBEGPPFCNPFVLTTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734

RESULT 6
Q8N2E1 PRELIMINARY; PRT; 477 AA.
AC Q8N2E1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein P8EC0226.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Iwagai T.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
R_ EMBL; AK075527; BAC11672.1; -.
DR HSP; Q90240; IHL8.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR000834; Peptidase M14.
DR Pfam; PF00754; F5_F8 type C; 1.
DR Pfam; PF00246; Zn_CarboxPept; 1.
DR PRINTS; PR00765; CB0XPYAFSEA.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS50022; FA58C_3; 1.
KW Carboxypeptidase.
SQ SEQUENCE 477 AA; 52766 MW; 0A3FBEA77B57A246 CRC64;

Query Match 81.1%; Score 2491; DB 2; Length 477;
Best Local Similarity 99.8%; Pred. No. 9e-174;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MWGLLLAALFAAPAVGALGAPRNVLGLAQPTTKVPGSTPALHSSPAQPAETANGTS 60
Db 1 MWGLLLAALFAAPAVGALGAPRNVLGLAQPTTKVPGSTPALHSSPAQPAETANGTS 60
Qy 61 EQHVRIRVKKKKVIMKKKKLTLRPTPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120
Db 61 EQHVRIRVKKKKVIMKKKKLTLRPTPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120
Qy 121 ESLRVSDSLSEASSQSFGLGPHRGLNIQSGLDGLYDGAACAEQDAPFWFQVDAGH 180
Db 121 ESLRVSDSLSEASSQSFGLGPHRGLNIQSGLDGLYDGAACAEQDAPFWFQVDAGH 180
Qy 181 PFRFSGVITQGRNSVWRVDWVTSYKVFQSNDSRTWWSGRNHSNGMDVFPANSDPETVL 240
Db 181 PFRFSGVITQGRNSVWRVDWVTSYKVFQSNDSRTWWSGRNHSNGMDVFPANSDPETVL 240
Qy 241 NLLPPEQVARFRLLLPQTWLOGAPCLRAEILACVPSPDNDLFLFAPASGSSDPLDFQHH 300
Db 241 NLLPPEQVARFRLLLPQTWLOGAPCLRAEILACVPSPDNDLFLFAPASGSSDPLDFQHH 300

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Qy 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHELGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHELGEPEVRYVAGMH 360
Qy 361 GNEALGRELLLLLMQFLCHEFLRGPNVTRLLSENRHLLPSMNDGVEIAYHRGSELVG 420
Db 361 GNEALGRELLLLLMQFLCHEFLRGPNVTRLLSENRHLLPSMNDGVEIAYHRGSELVG 420
Qy 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODDGKVPHPHVNHHPLP 465
Db 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODDGKVPHPHVNHHPLP 465

RESULT 7
CPXM_MOUSE
ID CPXM_MOUSE STANDARD; PRT; 722 AA.
AC Q9Z100; Q99LA3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potential carboxypeptidase X precursor (EC 3.4.17.-)
DE (Metalloproteinase)
DE (Metalloproteinase)
GN Name=Cpxm; Synonyms=Cpxm1, Cpx1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Heart;
RX MEDLINE=99171585; PubMed=10073577;
RA Lei Y., Xin X., Morgan D., Pintar J.E., Fricker L.D.;
RT "Identification of mouse CPX-1, a novel member of the
RT metalloproteinase gene family with highest similarity to CPX-
RT 2."
RL DNA Cell Biol. 18:175-185 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Feihly J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: May be involved in cell-cell interactions. No
CC carboxypeptidase activity was found yet.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Strongly expressed in testis and spleen.
CC Moderately expressed in salivary gland, brain, heart, lung, and
CC kidney. Extremely low expression in liver and adipose tissue.
CC -1- DEVELOPMENTAL STAGE: First expressed at 13.5 dpc, in the meninges,
CC nasal mesenchyme, primordial cartilage and skeletal structures.
CC -1- SIMILARITY: Belongs to peptidase family M14.
CC -1- SIMILARITY: Contains 1 F5/8 type C domain.

```









Db 597 TVAGSLNDFSYLHNTCPFLSIYVGDYKYPHSELPEWENNRESLIIVFMEQVHRIGKIV 656  
 Qy 511 -----VTASAEGVHSVTRNCRTVFE 530  
 Db 657 RDLQKGISNAVISVEGVNHDIRTSADGDYWRLLNPGYVVTAKAEGFISTKNCWGYD 716  
 Qy 531 EGPPFCNFVLTKPKQRLRELLAAGAKVPPDLRRRLRLRQOK 573  
 Db 717 MGATRCDFTLTKTNLARIREIMETFGKQVSLPSRLKLRGRK 759

RESULT 9  
 CPX2 HUMAN STANDARD; PRT; 756 AA.  
 AC Q8N436;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Potential carboxypeptidase-like protein X2 precursor (UNQ676/PRO1310).  
 GN Name=CPXM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;  
 RA "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain, and Lung;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deirge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: May be involved in cell-cell interactions.  
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -!- SIMILARITY: Belongs to peptidase family M14.  
 CC -!- SIMILARITY: Contains 1 F5/8 type C domain.  
 CC -!- CAUTION: As it has lost active sites residues and zinc-binding  
 CC sites it is unlikely to be catalytically active.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL; AY358565; AAQ8928.1; -;  
 DR EMBL; BC036789; AAH36789.1; ALT\_INIT.  
 DR HSP; O90240; IHL8L.  
 DR MEROPS; M14.019; -;  
 DR InterPro; IPR008969; CarboxypepD\_reg.  
 DR InterPro; IPR000421; FAS8\_C.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000834; Peptidase\_M14.  
 DR InterPro; IPR008575; Peptidase\_M14B.  
 DR Pfam; PF05885; DUF857; 1.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 1.  
 DR Pfam; PF00246; Zn\_carboxypept; 1.  
 DR PRINTS; PR00765; CRBOXYPTASEA.  
 DR SMART; SM00231; FAS8C; 1.  
 DR SMART; SM00631; Zn\_pept; 1.  
 DR PROSITE; PS00132; CARBOXYPEPT\_ZN\_1; 1.  
 DR PROSITE; PS01285; FAS8C\_1; 1.  
 DR PROSITE; PS01286; FAS8C\_2; 1.  
 DR PROSITE; PS50022; FAS8C\_3; 1.  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 25 Potential.  
 FT CHAIN 26 756 Potential carboxypeptidase-like protein  
 FT X2,  
 FT F5/8 type C.  
 FT DOMAIN 134 293 Pro-rich.  
 FT DOMAIN 45 101 Poly-Leu.  
 FT DISULFID 136 293 By similarity.  
 FT CARBOHYD 231 231 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 281 281 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 491 491 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 756 AA; 85897 MW; 1A2F1A5BA7C1DB6E CRC64;  
 Query Match 45.3%; Score 1390.5; DB 1; Length 756;  
 Best Local Similarity 40.0%; Pred. No. 6.1e-93;  
 Matches 299; Conservative 76; Mismatches 185; Indels 187; Gaps 8;  
 Qy 4 LLLAALAPAVGPAALGAP-----RNSVLGLAQPGTKVPGSTPALHSSPAQPAE 54  
 Db 15 LLAVTLAGVGAQAALDDFYQEIWSREPYARPEP---ELETSPPL---PAGEEE 69  
 Qy 55 TANGTSEQHVRIRVIKKKVIKKRKLTLTRPTPLVLTAGPLVTPT----PAGTLPDA-- 108  
 Db 69 WERRPQEPRPKPKKPKKA--PKREKSAPEPPPGKHSNKKVMRTKSEKAANDDSVR 126  
 Qy 109 ---EKOETGCPPLGLSLRVSRLRLEASSQSFGLGPHGRGLNIQSGLEDGLYDGAWCA 165  
 Db 127 VAREDVRESCPPLGLETLKITDQLHASTVKRYGLGAHRGLNIQAGINENDFYDGAWCA 186  
 Qy 166 EEOADPWQVDAGHPTRESGVITQGRNSVWRVDWVTSYKVFQSNDSRTWGSRNHSSGM 225  
 Db 187 GRNDLQWLVEVDARRLTRGTGITQGRNSLWLSWDVTSYKVMVNSDHTVTVTVNGSG-- 244  
 Qy 226 DAVFPANSDPETPVLMLLPQVAREIRLLPQTLQGGAPCLRAETLACVPSPNDLFLFLE 285  
 Db 245 DMIFEGNSEKEIPVLNELPVPVARYIRINPQSWFNGSICMERMEITLGCPLDPNNYHR 304  
 Qy 286 APASGSSDPLDFQHNYKAMKMLKQVQCCPNITRIYSIGKSYQGLKLYVMMSKPGGE 345  
 Db 305 RNEMTTTDDLDFKHHYKEMRQMLKVMVNMCPNITRIYINIGKSHQGLKLYAVEISHPGE 364  
 Qy 346 HELGEPEVYVAGMHGNEALGRELILLMLQFLCHEFLRGNPRVTRILLSEMRHLLPSMNP 405  
 Db 365 HEVGEPEFYIAGAHGNEVLGRELILLMLQFLCHEFLRGNPRVTRILLSEMRHLLPSMNP 424  
 Qy 406 DGVEIAYHRGSELVGVWAEGRWNNQSIDLNNHFNADLTPLWEAQDDGKVPHIVPNHPLP 465





DE	Aortic carboxypeptidase-like protein ACPLP.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
[1]	
SEQUENCE FROM N.A.	
TISSUE=Aorta smooth muscle;	
MDL=98288305; PubMed=9624159;	
Wayne M.D., Edge W.O., Jain M.K., Yet S.F., Hsieh C.M., Chin M.T.,	
Perrella M.A., Blann M.A., Haber E., Lee M.E.;	
"Aortic carboxypeptidase-like protein, a novel protein with discoidin	
and carboxypeptidase-like domains, is up-regulated during vascular	
smooth muscle cell differentiation.";	
J. Biol. Chem. 273:15654-15660(1998).	
EMBL; AF053944; AAC25985.1; -.	
PIR; JC5256; JC5256.	
HSSP; Q90240; IH8L.	
MEROPS; M14_951; -.	
Genew; HGNC:303; AEBP1.	
GO; GO:0004180; F:carboxypeptidase activity; TAS.	
GO; GO:0003700; F:transcription factor activity; TAS.	
GO; GO:0007517; P:muscle development; TAS.	
GO; GO:0001501; P:skeletal development; TAS.	
InterPro; IPR000421; FA58_C.	
InterPro; IPR008979; Gal_bind_like.	
InterPro; IPR000834; Peptidase_M14.	
InterPro; IPR008575; Peptidase_M14B.	
Pfam; PF05885; DUF857; 1.	
Pfam; PF00754; F5_P8_type_C; 1.	
Pfam; PF00246; Zn_carbopept; 1.	
PRINTS; PR00765; GBQXYPTASEA.	
SMART; SM00231; FA58C; 1.	
SMART; SM00631; Zn_pept; 1.	
PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.	
PROSITE; PS01285; FA58C_1; 1.	
PROSITE; PS01286; FA58C_2; UNKNOWN_1.	
PROSITE; PS50022; FA58C_3; 1.	
Carboxypeptidase.	
SEQUENCE 1158 AA; 130901 MW; 3BFC06B6A4971F30 CRC64;	
Query Match 38.0%; Score 1166; DB 2; Length 1158;	
Best Local Similarity 37.7%; Pred. No. 3e-76;	
Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8	
QY 107 PAEQETGCPPLGLESURVSDRLEASSQSFGLGPHGRNLNQSLEDGLYDGAWCAE 166	
DB 379 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRLLNMQTGATEDYDYGAWCAE 436	
QY 167 EQDADPWFQVDAGHPTRFSGVITQGRNSVMRYDYWTSYKVQFNSDRTWGSRHSSGMD 226	
DB 437 DDARTQIEWDTRTTRTGTGVTQGRDSSIHDDFTVTTFVGFNSDSQITVMVTNGYEEM- 495	
QY 227 AVFPANSDPETFVLNLLPEPQVAPRIURLPOTWLOGGAPCTRAETIACPVSDPNDLFLEA 286	
DB 496 -TFHGNVDKDPVLSELPEPVVAPRIYPLTW--NGSLCMRLEVLGGSVAPVYSYAQN 552	
QY 287 PASGSSDPLDQHHNYKAWKMLMKOVQCCNITRIYSIGSKSYQGLKLYVMEMSDKPEH 346	
DB 553 EVV-ATDDLDPRHHSYKDMRQLMKVNBECPTITRTYSLGKSSRGKLIYAMEISDNPGEH 611	
QY 347 ELGPEPVRYVAGMHGNEALGRELILLMLQFLCHEFLRGNPRVTRLISEMRIHLPSMNP 406	
DB 612 ELGPEFRTAGIHGNEVLGRELLILLMLQYLCREYRDGNPRVRSVLQDTRIHLVPSLNP 671	
QY 407 GYEIAYHRGSELVHGAEGRWNNQSDILNHNFADINTPLWEAQDQGVPHIVHNHLLPPT 466	
DB 672 GYEVAQQMGSEFGNWALGLWTEEGFDIFEDFPLNSVLWGAERKWPVRYVNNNLPIPE 731	
QY 467 YVTLPNATVAPETRAVIKWKRIIPVLISANLHGGELVWSYPDM----- 510	
DB 732 RYLSFDAVTSVEVRAIIAWMEKNPVLGNLNGGERLVSYPYDMARTPTOEQLLAAMAA 791	

DR	InterPro; IPR008575; Peptidase_M14B.	DE	Transcription factor AEBP1.
DR	Pfam; PF05885; DUF857; 1.	OS	Bos taurus (Bovine).
DR	Pfam; PF00754; F5_F8_type_C; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	Pfam; PF00246; Zn_Carboxypept; 1.	OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
DR	PRINTS; PR00765; CRBOXYPTASEA.	OC	Bovinae; Bos.
DR	SMART; SM00231; FA58C; 1.	OX	NCBI_TaxID=9913;
DR	SMART; SM00631; Zn_pept; 1.	RN	[1]
DR	PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.	RP	SEQUENCE FROM N.A.
DR	PROSITE; PS01285; FA58C_1; 1.	RC	TISSUE=Articular cartilage;
DR	PROSITE; PS01286; FA58C_2; UNKNOWN_1.	RA	Flory D.M., Kollar J., Huynh T.D., Hering T.M.;
DR	PROSITE; PS50022; FA58C_3; 1.	RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR	SEQUENCE 1158 AA; 130928 MW; 1D7F4A20451646AE CRC64;	DR	EMBL; AF043942; AAD02283.1; -.
DR		DR	HSSP; Q90240; 1H8L.
DR		DR	MEROPS; M14_951; -.
DR		DR	GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR		DR	GO; GO:0008270; F:zinc ion binding; IEA.
DR		DR	GO; GO:0007155; P:cell adhesion; IEA.
DR		DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR		DR	InterPro; IPR008969; Carboxypept_reg.
DR		DR	InterPro; IPR00421; FA58 C.
DR		DR	InterPro; IPR008979; Gal_bind like.
DR		DR	InterPro; IPR000834; Peptidase_M14.
DR		DR	InterPro; IPR008575; Peptidase_M14B.
DR		DR	Pfam; PF05885; DUF857; 1.
DR		DR	Pfam; PF00754; F5_F8_type_C; 1.
DR		DR	Pfam; PF00246; Zn_Carboxypept; 1.
DR		DR	PRINTS; PR00765; CRBOXYPTASEA.
DR		DR	SMART; SM00231; FA58C; 1.
DR		DR	SMART; SM00631; Zn_pept; 1.
DR		DR	PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR		DR	PROSITE; PS01285; FA58C_1; 1.
DR		DR	PROSITE; PS01286; FA58C_2; UNKNOWN_1.
DR		DR	PROSITE; PS50022; FA58C_3; 1.
DR		SQ	SEQUENCE 728 AA; 82355 MW; 63D356304C90C96D CRC64;
DR			
DR		Query Match	35.0%; Score 1073; DB 2; Length 728;
DR		Best Local Similarity	37.0%; Pred. No. 1e-69;
DR		Matches 226; Conservative	71; Mismatches 122; Indels 192; Gaps 6
Qy	149 IOSGLDGLYDGCACAEQDADPMFOVDAGHPTFRFSGVITQGRNSVMRYDMVTSYKVOF	Qy	149 IOSGLDGLYDGCACAEQDADPMFOVDAGHPTFRFSGVITQGRNSVMRYDMVTSYKVOF
Db	1 MQAGTEDDYDGCACAEDDSDQTIWEDTRTTKFTGVTIQRDSSIHDDFVTSFFVGF	Db	1 MQAGTEDDYDGCACAEDDSDQTIWEDTRTTKFTGVTIQRDSSIHDDFVTSFFVGF
Qy	209 Sndsrtwmsgrhssgmdavfpansdpptvlnllpepovarfirllpqlpqlqgacplr	Qy	209 Sndsrtwmsgrhssgmdavfpansdpptvlnllpepovarfirllpqlpqlqgacplr
Db	61 Sndsqtwmvmtngyem--TFHGNVDKOTPVLSPEPVPVAFRIYPLTW--NGSLCWR	Db	61 Sndsqtwmvmtngyem--TFHGNVDKOTPVLSPEPVPVAFRIYPLTW--NGSLCWR
Qy	269 AEILACVPSDPNDLFLAEAPASGSDPLDFQHNYKAMKMKVQEQCPNTRIYSIGKS	Qy	269 AEILACVPSDPNDLFLAEAPASGSDPLDFQHNYKAMKMKVQEQCPNTRIYSIGKS
Db	117 LEVLGCPVSPVHSYAQNEW--TTDDLPFRHNYKDMRQMKVNVNQCPNTRIYSIGKS	Db	117 LEVLGCPVSPVHSYAQNEW--TTDDLPFRHNYKDMRQMKVNVNQCPNTRIYSIGKS
Qy	329 YQGLKLYVMEMDKGEHELGEPEVRYVAGHGEALGRELILLMQLFCHFLRGDPRV	Qy	329 YQGLKLYVMEMDKGEHELGEPEVRYVAGHGEALGRELILLMQLFCHFLRGDPRV
Db	176 SRGLKTYAMEISDNPGDHGELGEPFERYTAGIHGNEVLGRELILLMQLFCHFLRGDPRV	Db	176 SRGLKTYAMEISDNPGDHGELGEPFERYTAGIHGNEVLGRELILLMQLFCHFLRGDPRV
Qy	389 TRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVAGHGEALGRELILLMQLFCHFLRGDPRV	Qy	389 TRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVAGHGEALGRELILLMQLFCHFLRGDPRV
Db	236 RSLVQDTRHLVPSLNPDGYEVAQAQMGSEFGNWLGLWTEGDFDIYEDFPDVSVLWGA	Db	236 RSLVQDTRHLVPSLNPDGYEVAQAQMGSEFGNWLGLWTEGDFDIYEDFPDVSVLWGA
Qy	449 DQGVPHIVPNHHLPLPTTYTLPLNATVAPETRAVTKWMKRIPFVLSANLHGELVVSYPF	Qy	449 DQGVPHIVPNHHLPLPTTYTLPLNATVAPETRAVTKWMKRIPFVLSANLHGELVVSYPF
Db	296 ERKWVPYRVNNLPIPERYLSPDATVSTEVRAIIAMWKNPFLVLANGLNGERLVSYPY	Db	296 ERKWVPYRVNNLPIPERYLSPDATVSTEVRAIIAMWKNPFLVLANGLNGERLVSYPY
Qy	509 DM-----	Qy	509 DM-----
Db	356 DMARTSQBQLAAAMAAARGEDBEVSEAQETPDHAIFRWLAIASFASHLTMTPEYRG	Db	356 DMARTSQBQLAAAMAAARGEDBEVSEAQETPDHAIFRWLAIASFASHLTMTPEYRG
Qy	511 -----	Qy	511 -----
Db	416 CQADYTGGMGIINGAKWKPRSGTINDFSYLHNTCLLSIFLGCDKFPHESELPREWNN	Db	416 CQADYTGGMGIINGAKWKPRSGTINDFSYLHNTCLLSIFLGCDKFPHESELPREWNN
Qy	511 -----	Qy	511 -----

RESULT 15
097567
ID 097567
AC 097567
DT 01-MAR
DT 01-MAR
DT 01-OCT

Db 476 KEALLTFMEQVHRGIGKGVVTDEQGIPIANATISVSGINHGVTASGGDYWRILNPGERYV 535  
Qy 512 TASAEQYHSVTRNCRVTFEBGPFPCNEVLTKTPKQRLRELLAAGAKVP-PDL----- 562  
Db 536 TAHAEGYTPSSKTCNVVDYDIGATOCNFILARSNWKRIREIMAMNGNRPIPRIDPSRPMT 595  
Qy 563 -RRRLRLRGQ 572  
Db 596 QOREMQRRRLQ 606

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Job time : 210 secs